



results of BLAST

BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1091209372-21435-212177256124.BLASTQ4

Query= gi|3387911|gb|AAC28637.1| 2-oxoglutarate carrier protein
[Homo sapiens]
(314 letters)

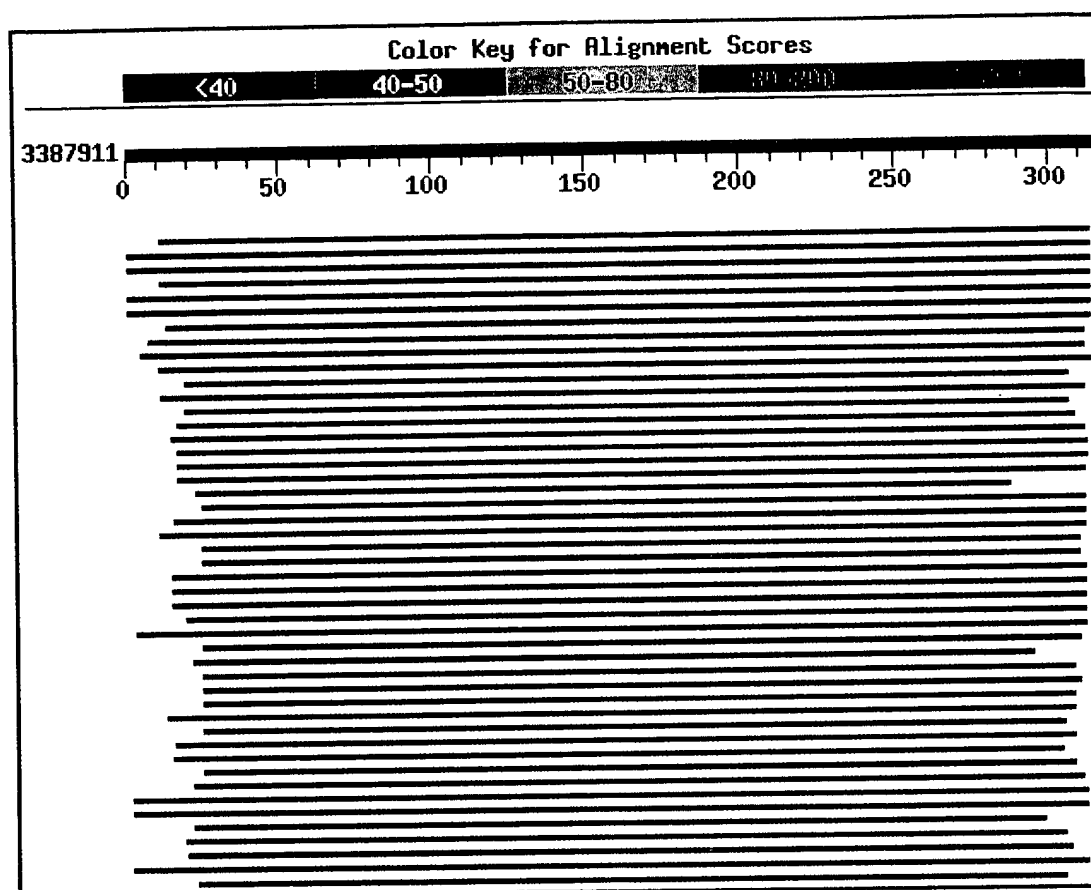
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
1,958,132 sequences; 658,882,765 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 140 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 21361114 ref NP_003553.2	solute carrier family 25 (mito...	590	e-167	L
gi 1580888 prf 2116232A	2-oxoglutarate carrier protein	588	e-167	
gi 21312994 ref NP_077173.1	solute carrier family 25 (mito...	588	e-167	L
gi 1079478 pir A56650	2-oxoglutarate carrier protein - hum...	588	e-167	L
gi 27807211 ref NP_777096.1	solute carrier family 25 (mito...	587	e-166	L
gi 11693170 ref NP_071793.1	2-oxoglutarate carrier [Rattus...	584	e-166	L
gi 47937747 gb AAH72308.1	MGC82600 protein [Xenopus laevis]	537	e-151	L
gi 50344854 ref NP_001002099.1	zgc:86898 [Danio rerio] >gi...	531	e-150	L
gi 47207195 emb CAF90256.1	unnamed protein product [Tetrao...	520	e-146	
gi 12834931 dbj BAB23092.1	unnamed protein product [Mus mu...	481	e-135	L
gi 7494946 pir T25459	hypothetical protein B0432.4 - Caeno...	407	e-112	
gi 39586904 emb CAE62839.1	Hypothetical protein CBG07018 [...	405	e-112	
gi 32564064 ref NP_493694.2	carrier (33.3 kD) (2A577) [Cae...	402	e-111	L
gi 31240035 ref XP_320431.1	ENSANGP00000016898 [Anopheles ...	358	1e-97	
gi 21358457 ref NP_651703.1	CG1907-PA [Drosophila melanoga...	348	8e-95	L
gi 20151395 gb AAM11057.1	GH11346p [Drosophila melanogaster]	329	6e-89	L
gi 24657951 ref NP_647924.2	CG18418-PA [Drosophila melanog...	329	6e-89	L
gi 24657945 ref NP_647923.1	CG7514-PA [Drosophila melanoga...	299	5e-80	L
gi 48133286 ref XP_393335.1	similar to CG5076-PA [Apis mel...	238	1e-61	L
gi 2130090 pir S65040	2-oxoglutarate/malate translocator (...	226	4e-58	

gi 2130089 pir S65042	2-oxoglutarate/malate translocator (...)	225	1e-57	
gi 23489162 gb EAA21506.1	putative oxoglutarate/malate tra...	224	2e-57	
gi 37964368 gb AAR06239.1	dicarboxylate/tricarboxylate car...	224	2e-57	
gi 15241167 ref NP_197477.1	dicarboxylate/tricarboxylate c...	224	3e-57	
gi 19913107 emb CAC84546.1	dicarboxylate/tricarboxylate ca...	221	2e-56	
gi 10798640 emb CAC12820.1	mitochondrial 2-oxoglutarate/ma...	221	2e-56	
gi 19913105 emb CAC84545.1	dicarboxylate/tricarboxylate ca...	220	3e-56	
gi 7489246 pir T07405	oxoglutarate/malate translocator - p...	217	2e-55	
gi 19913109 emb CAC84547.1	dicarboxylate/tricarboxylate ca...	217	3e-55	
gi 23612776 ref NP_704315.1	oxoglutarate/malate translocat...	215	1e-54	
gi 38101905 gb EAA48805.1	hypothetical protein MG00463.4 [...]	213	4e-54	
gi 15227225 ref NP_179836.1	mitochondrial substrate carrie...	209	6e-53	
gi 49097862 ref XP_410391.1	hypothetical protein AN6254.2 ...	206	4e-52	
gi 21554157 gb AAM63236.1	putative mitochondrial dicarboxy...	206	7e-52	
gi 13878155 gb AAK44155.1	putative mitochondrial dicarboxy...	205	1e-51	
gi 15233884 ref NP_194188.1	mitochondrial substrate carrie...	204	2e-51	
gi 50545838 ref XP_500457.1	hypothetical protein [Yarrowia...	204	3e-51	
gi 49088466 ref XP_406054.1	hypothetical protein AN1917.2 ...	201	1e-50	
gi 46806315 dbj BAD17507.1	2-oxoglutarate carrier-like pro...	201	2e-50	
gi 32407105 ref XP_324149.1	hypothetical protein [Neurospo...	201	2e-50	
gi 24637836 gb AAN63885.1	brain mitochondrial carrier prot...	197	3e-49	L
gi 24637838 gb AAN63886.1	brain mitochondrial carrier prot...	196	4e-49	L
gi 46127995 ref XP_388551.1	hypothetical protein FG08375.1...	196	9e-49	
gi 50423171 ref XP_460166.1	unnamed protein product [Debar...	195	1e-48	
gi 20149598 ref NP_036272.2	solute carrier family 25 (mito...	194	2e-48	L
gi 50745529 ref XP_420143.1	PREDICTED: similar to solute c...	193	5e-48	
gi 6179584 emb CAB59892.1	dicarboxylate carrier protein [H...	193	5e-48	L
gi 6755544 ref NP_035528.1	solute carrier family 25 (mitoc...	193	5e-48	L
gi 20141977 sp Q9Z2B2 UCP5 MOUSE	Brain mitochondrial carrie...	193	5e-48	L
gi 19173788 ref NP_596909.1	solute carrier family 25 (mito...	192	6e-48	L
gi 31207583 ref XP_312758.1	ENSANGP00000020409 [Anopheles ...]	192	9e-48	
gi 7274398 gb AAF44754.1	2-oxoglutarate/malate carrier [Ov...	192	1e-47	L
gi 13259543 ref NP_073721.1	solute carrier family 25, memb...	191	2e-47	L
gi 4507009 ref NP_003942.1	solute carrier family 25, membe...	191	2e-47	L
gi 12841977 dbj BAB25425.1	unnamed protein product [Mus mu...	191	2e-47	
gi 7768837 dbj BAA95593.1	brain mitochondrial carrier prot...	190	3e-47	L
gi 39586739 emb CAE65781.1	Hypothetical protein CBG10876 [...]	190	3e-47	
gi 17865339 ref NP_445953.1	solute carrier family 25 (mito...	190	4e-47	L
gi 32414947 ref XP_327953.1	probable dicarboxylate carrier...	190	4e-47	
gi 46109132 ref XP_381624.1	hypothetical protein FG01448.1...	189	5e-47	
gi 41055825 ref NP_956458.1	similar to solute carrier fami...	189	6e-47	L
gi 20137668 sp Q9QZD8 DIC MOUSE	Mitochondrial dicarboxylate...	189	6e-47	L
gi 7305501 ref NP_038798.1	solute carrier family 25 (mitoc...	189	6e-47	L
gi 17568881 ref NP_509133.1	oxoglutarate/malate carrier pr...	188	2e-46	L
gi 16041817 gb AAH15797.1	SLC25A10 protein [Homo sapiens]	187	3e-46	L
gi 25295877 pir T51899	probable 2-oxoglutarate/malate tran...	186	6e-46	
gi 21357545 ref NP_650279.1	CG8790-PA [Drosophila melanoga...	186	6e-46	L
gi 39722382 emb CAE84416.1	putative DIC1 protein [Pichia a...	184	3e-45	
gi 47123004 gb AAH70665.1	MGC82285 protein [Xenopus laevis]	183	4e-45	L
gi 46440994 gb EAL00295.1	hypothetical protein Ca019.5628 ...	183	4e-45	
gi 15242423 ref NP_196509.1	mitochondrial substrate carrie...	180	3e-44	
gi 41055124 ref NP_957466.1	similar to solute carrier fami...	180	4e-44	L
gi 15223098 ref NP_172866.1	mitochondrial substrate carrie...	179	5e-44	

gi 49069984 ref XP_399281.1	hypothetical protein UM01666.1...	179	7e-44	
gi 11094337 gb AAG29583.1	mitochondrial uncoupling protein...	176	5e-43	L
gi 47218453 emb CAG03725.1	unnamed protein product [Tetrao...	176	6e-43	
gi 13259162 gb AAK16829.1	mitochondrial uncoupling protein...	175	9e-43	
gi 38969885 gb AAH63207.1	LOC394840 protein [Xenopus tropi...	175	1e-42	L
gi 16755900 gb AAL28138.1	uncoupling protein UCP [Meleagri...	174	2e-42	
gi 47222581 emb CAG02946.1	unnamed protein product [Tetrao...	174	2e-42	
gi 45383892 ref NP_989438.1	uncoupling protein 3 (mitochon...	174	3e-42	L
gi 19913111 emb CAC84548.1	dicarboxylate/tricarboxylate ca...	173	4e-42	
gi 49116948 gb AAH72926.1	Unknown (protein for MGC:80420) ...	173	5e-42	
gi 22775580 dbj BAC15532.1	uncoupling protein [Gallus gallus]	173	6e-42	L
gi 33114697 gb AAP94991.1	uncoupling protein 3 [Dicrostony...	172	6e-42	
gi 49075182 ref XP_401675.1	hypothetical protein UM04060.1...	172	8e-42	
gi 6678495 ref NP_033490.1	uncoupling protein 3, mitochond...	172	9e-42	L
gi 18424178 ref NP_568894.1	uncoupling protein (UCP2) [Ara...	172	9e-42	
gi 13385736 ref NP_080508.1	solute carrier family 25, memb...	172	9e-42	L
gi 6323381 ref NP_013452.1	Mitochondrial dicarboxylate car...	172	1e-41	
gi 42742053 gb AAS45212.1	mitochondrial uncoupling protein...	172	1e-41	
gi 28849931 ref NP_776635.1	uncoupling protein 3 (mitochon...	171	2e-41	L
gi 4928052 gb AAD33396.1	uncoupling protein 3 [Sus scrofa]	171	2e-41	L
gi 50730839 ref XP_417040.1	PREDICTED: hypothetical protei...	171	3e-41	
gi 27881739 gb AAH44682.1	Ucp2-prov protein [Xenopus laevis]	170	4e-41	L
gi 47522914 ref NP_999214.1	uncoupling protein 3 [Sus scro...	170	4e-41	L
gi 7110733 ref NP_037299.1	uncoupling protein 3; Uncouplin...	170	4e-41	L
gi 49533767 gb AAT66766.1	putative mitochondrial uncouplin...	170	5e-41	
gi 11277066 pir T49628	probable dicarboxylate carrier prot...	169	1e-40	
gi 14195284 sp Q9N2I9 UCP3 CANFA	Mitochondrial uncoupling p...	168	2e-40	L

Alignments

>gi|21361114|ref|NP_003553.2| L solute carrier family 25 (mitochondrial carrier; o
carrier), member 11; solute carrier family 20
(oxoglutarate carrier), member 4 [Homo sapiens]
gi|20141580|sp|Q02978|M2OM HUMAN L Mitochondrial 2-oxoglutarate/malate carrier pr
gi|3387911|gb|AAC28637.1| L 2-oxoglutarate carrier protein [Homo sapiens]
gi|13676350|gb|AAH06508.1| L Solute carrier family 25 (mitochondrial carrier; oxo
carrier), member 11 [Homo sapiens]
gi|13676368|gb|AAH06519.1| L Solute carrier family 25 (mitochondrial carrier; oxo
carrier), member 11 [Homo sapiens]
gi|16740864|gb|AAH16294.1| L Solute carrier family 25 (mitochondrial carrier; oxo
carrier), member 11 [Homo sapiens]
gi|16877884|gb|AAH17170.1| L Solute carrier family 25 (mitochondrial carrier; oxo
carrier), member 11 [Homo sapiens]
gi|48145785|emb|CAG33115.1| SLC25A11 [Homo sapiens]
Length = 314

Score = 590 bits (1522), Expect = e-167
Identities = 303/303 (100%), Positives = 303/303 (100%)

Query: 12 IDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI 71
IDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI

Sbjct: 12 IDGKPRTSPKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI 71

Query: 72 LKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGA 131
LKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGA

Sbjct: 72 LKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGA 131

Query: 132 TGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARA 191
TGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARA

Sbjct: 132 TGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARA 191

Query: 192 VVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMR 251
VVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMR

Sbjct: 192 VVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMR 251

Query: 252 MIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFLEQMNKAYKRLF 311
MIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFLEQMNKAYKRLF

Sbjct: 252 MIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFLEQMNKAYKRLF 311

Query: 312 LSG 314
LSG

Sbjct: 312 LSG 314

>gi|1580888|prf||2116232A 2-oxoglutarate carrier protein
Length = 314

Score = 588 bits (1517), Expect = e-167
Identities = 304/314 (96%), Positives = 306/314 (97%)

Query: 1 MAATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTRE 60
MAATAS GAG +DGKPRTSPKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTRE

Sbjct: 1 MAATASPGAGRMDGKPRTSPKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTRE 60

Query: 61 YKTSFHALTSILKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFL 120
YKTSFHAL SILKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFL

Sbjct: 61 YKTSFHALISILKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFL 120

Query: 121 LKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTL 180
LKA+IGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRI REEGV TL

Sbjct: 121 LKALIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRIAREEGVPTL 180

Query: 181 WRGCIPTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPV 240
WRGCIPTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPV

Sbjct: 181 WRGCIPTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPV 240

Query: 241 DIAKTRIQNMRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFL 300
DI KTRIQNMRMIDGKPEYKNGLDVL KVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFL

Sbjct: 241 DIVKTRIQNMRMIDGKPEYKNGLDVLLKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFL 300

Query: 301 EQMNKAYKRLFLSG 314
EQMNKAYKRLFL G

Sbjct: 301 EQMNKAYKRLFLGG 314

>gi|21312994|ref|NP_077173.1| **L** solute carrier family 25 (mitochondrial carrier ox
carrier), member 11; solute carrier family 25
(mitochondrial carrier; oxoglutarate carrier), member 11
[Mus musculus]

gi|20138723|sp|Q9CR62|M2OM MOUSE **L** Mitochondrial 2-oxoglutarate/malate carrier pr
 gi|12844315|dbj|BAB26319.1| **L** unnamed protein product [Mus musculus]
 gi|12844856|dbj|BAB26524.1| **L** unnamed protein product [Mus musculus]
 gi|13097438|gb|AAH03455.1| **L** Solute carrier family 25 (mitochondrial carrier oxog
 carrier), member 11 [Mus musculus]
 gi|18043006|gb|AAH19631.1| **L** Solute carrier family 25 (mitochondrial carrier oxog
 carrier), member 11 [Mus musculus]
 Length = 314

Score = 588 bits (1517), Expect = e-167
 Identities = 303/314 (96%), Positives = 307/314 (97%)

Query: 1 MAATASAGAGGIDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60
 MAATAS GAG +DGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE
 Sbjct: 1 MAATASPGAGRMDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60
 Query: 61 YKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFL 120
 YKTSFHALTSILK EGL+GIYTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFL
 Sbjct: 61 YKTSFHALTSILKTEGLKGIYTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFL 120
 Query: 121 LKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLT 180
 LKA+IGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNAL+RI REEGV TL
 Sbjct: 121 LKALIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALVRIAREEGVPTL 180
 Query: 181 WRGCIPTMARAVVVNAAQLASYSQSKQFLDSGYFSDNILCHFCASMISGLVTTAASMPV 240
 WRGCIPTMARAVVVNAAQLASYSQSKQFLDSGYFSDNILCHFCASMISGLVTTAASMPV
 Sbjct: 181 WRGCIPTMARAVVVNAAQLASYSQSKQFLDSGYFSDNILCHFCASMISGLVTTAASMPV 240
 Query: 241 DIAKTRIQNMIRMIDGKPEYKNGLDVLFKVRYEGFFSLWKGFPPYARLGPHTVLTFIFL 300
 DI KTRIQNMIRMIDGKPEYKNGLDVL KVVRYEGFFSLWKGFPPYARLGPHTVLTFIFL
 Sbjct: 241 DIVKTRIQNMIRMIDGKPEYKNGLDVLLKVRYEGFFSLWKGFPPYARLGPHTVLTFIFL 300
 Query: 301 EQMNKAYKRLFLSG 314
 EQMNKAYKRLFLSG
 Sbjct: 301 EQMNKAYKRLFLSG 314

>gi|1079478|pir||A56650 2-oxoglutarate carrier protein - human
 gi|23844|emb|CAA46905.1| **L** 2-oxoglutarate carrier [Homo sapiens]
 Length = 314

Score = 588 bits (1517), Expect = e-167
 Identities = 302/303 (99%), Positives = 303/303 (100%)

Query: 12 IDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI 71
 +DGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI
 Sbjct: 12 MDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI 71
 Query: 72 LKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGA 131
 LKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGA
 Sbjct: 72 LKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGA 131
 Query: 132 TGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARA 191
 TGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARA
 Sbjct: 132 TGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARA 191
 Query: 192 VVVNAAQLASYSQSKQFLDSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMR 251

VVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMR
 Sbjct: 192 VVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMR 251

Query: 252 MIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLTFIFLEQMNKAYKRLF 311
 MIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLTFIFLEQMNKAYKRLF
 Sbjct: 252 MIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLTFIFLEQMNKAYKRLF 311

Query: 312 LSG 314
 LSG
 Sbjct: 312 LSG 314

>gi|27807211|ref|NP_777096.1| **L** solute carrier family 25 (mitochondrial carrier; o
 carrier), member 11 [Bos taurus]
 gi|126664|sp|P22292|M2OM BOVIN Mitochondrial 2-oxoglutarate/malate carrier protei
 gi|108460|pir|A36305 2-oxoglutarate/malate carrier protein, inner mitochondrial
 - bovine
 gi|32|emb|CAA46906.1| **L** 2-oxoglutarate carrier [Bos taurus]
 gi|163432|gb|AAA30671.1| **L** 2-oxoglutarate/malate carrier protein
 gi|163434|gb|AAA30672.1| **L** 2-oxoglutarate/malate carrier protein
 Length = 314

Score = 587 bits (1514), Expect = e-166
 Identities = 302/314 (96%), Positives = 305/314 (97%)

Query: 1 MAATASAGAGGIDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60
 MAATAS GA G+DGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE
 Sbjct: 1 MAATASPGASGMDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60

Query: 61 YKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTLGIYTVLFERLTGADGTPPGFL 120
 YKTSFHAL SIL+AEGLRGIYTGLSAGLLRQATYTTTTLGIYTVLFERLTGADGTPPGFL
 Sbjct: 61 YKTSFHALISILRAEGLRGIYTGLSAGLLRQATYTTTTLGIYTVLFERLTGADGTPPGFL 120

Query: 121 LKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLT 180
 LKAVIGMTAGATGAFVGTAEVALIRMTADGRLP DQRRGYKNVFNAL RI +EEGV TL
 Sbjct: 121 LKAVIGMTAGATGAFVGTAEVALIRMTADGRLPVDQRRGYKNVFNALFRIVQEEGVPTL 180

Query: 181 WRGCIPTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPV 240
 WRGCIPTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPV
 Sbjct: 181 WRGCIPTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPV 240

Query: 241 DIAKTRIQNMRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLTFIFL 300
 DI KTRIQNMRMIDGKPEYKNGLDVL KVVRYEGFFSLWKGFTPYARLGPHTVLTFIFL
 Sbjct: 241 DIVKTRIQNMRMIDGKPEYKNGLDVLVKVVRYEGFFSLWKGFTPYARLGPHTVLTFIFL 300

Query: 301 EQMNKAYKRLFLSG 314
 EQMNKAYKRLFLSG
 Sbjct: 301 EQMNKAYKRLFLSG 314

>gi|11693170|ref|NP_071793.1| **L** 2-oxoglutarate carrier [Rattus norvegicus]
 gi|2497985|sp|P97700|M2OM RAT Mitochondrial 2-oxoglutarate/malate carrier protein
 gi|1814078|gb|AAB41797.1| **L** 2-oxoglutarate carrier [Rattus norvegicus]
 Length = 314

Score = 584 bits (1505), Expect = e-166

Identities = 302/314 (96%), Positives = 304/314 (96%)

Query: 1 MAATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60
 MAATAS GAG +DGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLV NRMQLSGEGAKTRE
 Sbjct: 1 MAATASPGAGRMDGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVXNRMQLSGEGAKTRE 60

Query: 61 YKTSFHALTSILKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFL 120
 YKTSFHALTSILKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFL
 Sbjct: 61 YKTSFHALTSILKAEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFL 120

Query: 121 LKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTL 180
 LKA+IGMTAGATGAFVG PAEVALIRMTADGRLPADQRRGYKNVFNALIRI REEGV TL
 Sbjct: 121 LKALIGMTAGATGAFVGPPAEVALIRMTADGRLPADQRRGYKNVFNALIRIAREEGVPTL 180

Query: 181 WRGCIPTMARAVVVNAAQLASYSQSKQFLDLSGYFSDNILCHFCASMISGLVTTAASMPV 240
 WRGCIPTMARAVVVNAAQLASYSQSKQFLDLSGYFSDNILCHFCA MISGLVTTAASMPV
 Sbjct: 181 WRGCIPTMARAVVVNAAQLASYSQSKQFLDLSGYFSDNILCHFCAIMISGLVTTAASMPV 240

Query: 241 DIAKTRIQNMIRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPPYARLGPHTVLTFFIFL 300
 DI KTRIQNMIRMID KPEYKNGLDVLFKVVRYEGFFSLWKGFPPYARLGPHTVLTFFIFL
 Sbjct: 241 DIVKTRIQNMIRIDEKPEYKNGLDVLLKVVRYEGFFSLWKGFPPYARLGPHTVLTFFIFL 300

Query: 301 EQMNKAYKRLFLSG 314
 EQMNKAYKRLFLSG
 Sbjct: 301 EQMNKAYKRLFLSG 314

>gi|47937747|gb|AAH72308.1| **L** MGC82600 protein [Xenopus laevis]
 Length = 305

Score = 537 bits (1384), Expect = e-151
 Identities = 270/301 (89%), Positives = 284/301 (94%)

Query: 14 GKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILK 73
 G+ RTSPK+VKFLFGGLAGMGATVFVQPLDLVKNRMQLSG GAKT+EYKTSFHA+ SIL+
 Sbjct: 5 GRQRTSPKAVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGAGAKTKEYKTSFHAVGSILR 64

Query: 74 AEGLRGIYTGSLAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGATG 133
 EGLRGIYTGSLAGLLRQATYTTTTRLGIYT+LFE+ T ADGTPP F +KA IGMTAGATG
 Sbjct: 65 NEGLRGIYTGSLAGLLRQATYTTTTRLGIYITLFEKFTKADGTPPNFFMKAIGMTAGATG 124

Query: 134 AFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRGCIPTMARAVV 193
 AFVGTAEVALIRMTADGR+P DQRRGY NVFNAL+R+TREEG+ TLWRGCIPTMARAVV
 Sbjct: 125 AFVGTAEVALIRMTADGRMPVDQRRGYTNVFNALVRMTREEGITTLWRGCIPTMARAVV 184

Query: 194 VNAAQLASYSQSKQFLDLSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMIRMI 253
 VNAAQLASYSQSKQFLDLSGYF D+ILCHFCASMISGLVTTAASMPVDIAKTRIQNMIRMI
 Sbjct: 185 VNAAQLASYSQSKQFLDLSGYFRDDILCHFCASMISGLVTTAASMPVDIAKTRIQNMIRMI 244

Query: 254 DGKPEYKNGLDVLFKVVRYEGFFSLWKGFPPYARLGPHTVLTFFIFLEQMNKAYKRLFLS 313
 DGKPEYKNGLDVLFKVVRYEGFFSLWKGFPPYARLGPHTVLTFFIFLEQMNK YK FLS
 Sbjct: 245 DGKPEYKNGLDVLAKVVRYEGFFSLWKGFPPYARLGPHTVLTFFIFLEQMNKYKNFFLS 304

Query: 314 G 314
 G
 Sbjct: 305 G 305

>gi|50344854|ref|NP_001002099.1| **L** zgc:86898 [Danio rerio]
 gi|47939470|gb|AAH71521.1| **L** Zgc:86898 [Danio rerio]
 Length = 308

Score = 531 bits (1368), Expect = e-150
 Identities = 266/305 (87%), Positives = 281/305 (92%)

Query: 8 GAGGIDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHA 67
 A KP+TSPKS+KFLFGGLAGMGATVFVQPLDLVKNRMQLSG+G+K REYKTSFHA
 Sbjct: 2 AAAADTAKPKTSPKSIKFLFGGLAGMGATVFVQPLDLVKNRMQLSGQSKAREYKTSFHA 61

Query: 68 LTSILKAEGLRGIYTGLSAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPPGFLLKAVIGM 127
 + SIL+ EG+RGIYTGLSAGLLRQATYTTTTLRGIYT+LFRER++ ADGTPP F +KA+IGM
 Sbjct: 62 VGSILRNEGVVRIYTGLSAGLLRQATYTTTTLRGIYTILFERMSKADGTPPNFFMKALIGM 121

Query: 128 TAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRGCIPT 187
 TAGATGAFVGTAEVALIRMTADGRLP DQRRGY NVFNAL+RITREEGV TLWRGCIPT
 Sbjct: 122 TAGATGAFVGTAEVALIRMTADGRLPPDQRRGYTNVFNALVRITREEGVTTTLWRGCIPT 181

Query: 188 MARAVVVNAAQLASYSQSKQFLDSDGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRI 247
 MARAVVVNAAQLASYSQSKQ LLDSDGYF D+ILCHFCASMISGLVTTAASMPVDI KTRI
 Sbjct: 182 MARAVVVNAAQLASYSQSKQALLDSDGYFRDDILCHFCASMISGLVTTAASMPVDIVKTRI 241

Query: 248 QNMIRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFIFLEQMNKAY 307
 QNMIRMIDGKPEY NGLDVL KV+R EGFFSLWKGFPTPYARLGPHTVLTFIFLEQMNK Y
 Sbjct: 242 QNMIRMIDGKPEYNNGLDVLFKVRNEGVVRYEGFFSLWKGFPTPYARLGPHTVLTFIFLEQMNKAY 301

Query: 308 KRLFL 312
 K FL
 Sbjct: 302 KIYFL 306

>gi|47207195|emb|CAF90256.1| unnamed protein product [Tetraodon nigroviridis]
 Length = 313

Score = 520 bits (1339), Expect = e-146
 Identities = 264/312 (84%), Positives = 284/312 (91%), Gaps = 4/312 (1%)

Query: 5 ASAGAGGIDGKPRTPSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTS 64
 AS G D KP+TSPK++KFLFGGLAGMGATVFVQPLDLVKNRMQLSG+G K REY+TS
 Sbjct: 1 ASPGGMADTKPKTSPKAIKFLFGGLAGMGATVFVQPLDLVKNRMQLSGQGTKAREYRTS 60

Query: 65 FHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPPGFLLKAV 124
 FHAL SIL+ EG+ GIYTGLSAGLLRQATYTTTTLRGIYT+LFE++TG+DG PP F+LKA+
 Sbjct: 61 FHALFSILRNEGVVGIYTGLSAGLLRQATYTTTTLRGIYTILFEKMTGSDGRPPSFILKAL 120

Query: 125 IGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRGC 184
 IGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGY NVFNAL RI+REEGV TLWRGC
 Sbjct: 121 IGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYTNVFNALARISREEGVATLWRGC 180

Query: 185 IPTMARAVVVNAAQLASYSQSKQFLD---SGYFSDNILCHFCASMISGLVTTAASMPV 240
 +PTMARAVVVNAAQLASYSQSKQ LLD SGYF+D+ILCHFCASMISGLVTTAASMPV
 Sbjct: 181 VPTMARAVVVNAAQLASYSQSKQALLDPSGYFNDDILCHFCASMISGLVTTAASMPV 240

Query: 241 DIAKTRIQNMIRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFIFL 300
 DI KTRIQNMIRMIDGKPEYKNGL+VL +VVR EGFFSLWKGFPTPYARLGPHTVLTFIFL
 Sbjct: 241 DIVKTRIQNMIRMIDGKPEYKNGLEVLLRVVRSEGVVRYEGFFSLWKGFPTPYARLGPHTVLTFIFL 300

Query: 301 EQMNKAYKRLFL 312
 EQMN+ YK L
 Sbjct: 301 EQMNRLYKTYVL 312

>gi|12834931|dbj|BAB23092.1| **L** unnamed protein product [Mus musculus]
 Length = 252

Score = 481 bits (1239), Expect = e-135
 Identities = 244/252 (96%), Positives = 247/252 (98%)

Query: 63 TSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLK 122
 TSFHALTSILK EGL+GIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLK
 Sbjct: 1 TSFHALTSILKTEGLKGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLK 60

Query: 123 AVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWR 182
 A+IGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNAL+RI REEGV TLWR
 Sbjct: 61 ALIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALVRIAREEGVPTLWR 120

Query: 183 GCIPTMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDI 242
 GCIPTMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDI
 Sbjct: 121 GCIPTMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDI 180

Query: 243 AKTRIQNMRMIDGKPEYKNGLDVLFKVRYEGFFSLWKGFTPYARLGPHTVLTFFIFLEQ 302
 KTRIQNMRMIDGKPEYKNGLDVLFKVRYEGFFSLWKGFTPYARLGPHTVLTFFIFLEQ
 Sbjct: 181 VKTRIQNMRMIDGKPEYKNGLDVLLKVRYEGFFSLWKGFTPYARLGPHTVLTFFIFLEQ 240

Query: 303 MNKAYKRLFLSG 314
 MNKAYKRLFLSG
 Sbjct: 241 MNKAYKRLFLSG 252

Score = 52.8 bits (125), Expect = 1e-05
 Identities = 47/182 (25%), Positives = 74/182 (40%), Gaps = 6/182 (3%)

Query: 11 GIDGKPRTPSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGE--GAKTREYKTSFHAL 68
 G DG P +K L G AG P ++ RM G + R YK F+AL
 Sbjct: 49 GADGTP--PGFLLKALIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNAL 106

Query: 69 TSILKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMT 128
 I + EG+ ++ G + R +L Y+ + L + L M
 Sbjct: 107 VRIAREEGVPTLWRGCIPTMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMI 166

Query: 129 AGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRGCIPTM 188
 +G P ++ R+ + R+ D + YKN + L+++ R EG +LW+G P
 Sbjct: 167 SGLVTTAASMPVDIVKTRIQ-NMRM-IDGKPEYKNGLDVLLKVRYEGFFSLWKGFTPY 224

Query: 189 AR 190
 AR
 Sbjct: 225 AR 226

>gi|7494946|pir||T25459 hypothetical protein B0432.4 - Caenorhabditis elegans
 Length = 323

Score = 407 bits (1047), Expect = e-112
 Identities = 209/288 (72%), Positives = 232/288 (80%), Gaps = 2/288 (0%)

Query: 20 PKSVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRG 79
P VKF FGG AGMGAT+ VQPLDLVKNRMQLSG K +EY++S HALTSI+K EG+
Sbjct: 8 PNVVKFAFGGTAGMGATLVVQPLDLVKNRMQLSGTTGK-KEYRSSMHALTSIMKNEGVFA 66

Query: 80 IYTGLSAGLLRQATYTTTTLGLIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFVGTP 139
+Y GLSAGLLRQATYTTTTLGL Y L ER T D P F +KAV+GMTAG G+FVGTP
Sbjct: 67 VYNGLSAGLLRQATYTTTTLGLTYAFLLEFTEKD-KPLSFGMKAVLGMTAGGIGSFVGTP 125

Query: 140 AEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLTLWRGCIPTMARAVVVNAAQL 199
AE+ALIRMT DGRLP +QRR Y V NAL RIT+EEGVTLTLWRGC PT+ RA+VVNAAQL
Sbjct: 126 AEIALIRMTGDGRLPVEQRRNYTGVVNALTRITKEEGVTLTLWRGCTPTVLRAMVVNAAQL 185

Query: 200 ASYSQSKQFLLDSDGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGKPEY 259
A+YSQ+KQ LL SG D I CHF ASMISGL TT ASMPVDIAKTRIQ+M++IDGKPEY
Sbjct: 186 ATYSQAKQALLASGKVQDGIFCHFLASMISGLATTIASMPVDIAKTRIQSMKVIDGKPEY 245

Query: 260 KNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMNAAY 307
KN DV KV++ EG F+LWKGFPTPY RLGPHTVLTFFI LEQMN AY
Sbjct: 246 KNAFDVWGKVIKNEGIFALWKGFPTPYMRLGPHTVLTFFIILEQMNAAY 293

>gi|39586904|emb|CAE62839.1| Hypothetical protein CBG07018 [Caenorhabditis briggsa]
Length = 307

Score = 405 bits (1040), Expect = e-112
Identities = 210/301 (69%), Positives = 239/301 (79%), Gaps = 2/301 (0%)

Query: 12 IDGKPRTSPKSVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI 71
+ G+ T P +VKF FGG AGMGAT+ VQPLDLVKNRMQLSG K +EY++S HALTSI
Sbjct: 1 MSGETATVPNAVVKFAFGGTAGMGATLVVQPLDLVKNRMQLSGTTGK-KEYRSSMHALTSI 59

Query: 72 LKAEGLRGIYTGLSAGLLRQATYTTTTLGLIYTVLFRERLTGADGTPPGFLLKAVIGMTAGA 131
+K EG IY GLSAGLLRQATYTTTTLGL Y+ L E+ T D P F +KA +GM AG
Sbjct: 60 IKNEGFFAIYNGLSAGLLRQATYTTTTLGLTYSFLMEKFTEKD-KPLSFAMKAGLGMAAGG 118

Query: 132 TGAFVGTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLTLWRGCIPTMARA 191
G+FVGTPAE+ALIRMT DGRLP +QRR YK V NAL RIT+EEGVTLTLWRGC PT+ RA
Sbjct: 119 IGSFVGTPAELALIRMTGDGRLPQEQRRNYKGVVNALTRITKEEGVTLTLWRGCTPTVIRA 178

Query: 192 VVVNAAQLASYSQSKQFLLDSDGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMR 251
+VVNAAQLA+YSQ+KQ LL+SG D + CHF ASMISGL TT ASMPVDIAKTRIQ+M+
Sbjct: 179 MVVNAAQLATYSQAKQALLESQKQVQDGVFCHFLASMISGLATTIASMPVDIAKTRIQSMK 238

Query: 252 MIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMNAAYKRLF 311
+IDGKPEYKN DV KV++ EG F+LWKGFPTPY RLGPHTVLTFFI LEQMN AY +
Sbjct: 239 VIDGKPEYKNAFDVWGKVIKNEGIFALWKGFPTPYMRLGPHTVLTFFIILEQMNAAYKYV 298

Query: 312 L 312
L
Sbjct: 299 L 299

>gi|32564064|ref|NP_493694.2| L carrier (33.3 kD) (2A577) [Caenorhabditis elegans]
gi|24418292|gb|AAB37890.2| Hypothetical protein B0432.4 [Caenorhabditis elegans]
Length = 306

Score = 402 bits (1034), Expect = e-111

Identities = 209/288 (72%), Positives = 232/288 (80%), Gaps = 2/288 (0%)

Query: 20 PKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRG 79
 P VKF FGG AGMGAT+ VQPLDLVKNRMQLSG K +EY++S HALTSI+K EG+
 Sbjct: 8 PNVVKFAFGGTAGMGATLVVQPLDLVKNRMQLSGTTGK-KEYRSSMHALTSIMKNEGVFA 66

Query: 80 IYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFVGTP 139
 +Y GLSAGLLRQATYTTTTRLG Y L ER T D P F +KAV+GMTAG G+FVGTP
 Sbjct: 67 VYNGLSAGLLRQATYTTTTRLGTYAFLLERFTEKD-KPLSFGMKAVLGMTAGGIGSFVGTP 125

Query: 140 AEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLRGCIPTMARAVVVNAAQL 199
 AE+ALIRMT DGRLP +QRR Y V NAL RIT+EEGVLTWLRGC PT+ RA+VVNAAQL
 Sbjct: 126 AEIALIRMTGDGRLPVEQRRNYTGVVNALTRITKEEGVLTWLRGCTPTVLRAMVVNAAQL 185

Query: 200 ASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGKPEY 259
 A+YSQ+KQ LL SG D I CHF ASMISGL TT ASMPVDIAKTRIQ+M++IDGKPEY
 Sbjct: 186 ATYSQAKQALLASGKVQDGIFCHFLASMISGLATTIASMPVDIAKTRIQSMKVIDGKPEY 245

Query: 260 KNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMNKAY 307
 KN DV KV++ EG F+LWKGFPTPY RLGPHTVLTFFI LEQMN AY
 Sbjct: 246 KNAFDVWGKVIKNEGIFALWKGFPTPYMRLGPHTVLTFFIILEQMNAAAY 293

>gi|31240035|ref|XP_320431.1| ENSANGP00000016898 [Anopheles gambiae]
 gi|21288014|gb|EAA00335.1| ENSANGP00000016898 [Anopheles gambiae str. PEST]
 Length = 344

Score = 358 bits (918), Expect = 1e-97
 Identities = 177/294 (60%), Positives = 220/294 (74%), Gaps = 1/294 (0%)




Query: 17 RTSPKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAE 76
 + P V+++ GGL+G+GAT VQPLDLVK RMQ+SG G +EY +F A+ I++ EG
 Sbjct: 40 KKRPFVYVQYVLGGLSGIGATCVVQPLDLVKTRMQISGMGAAKEYNNTFDAIGKIMRREG 99

Query: 77 LRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFV 136
 + +Y GLSA ++RQATYTTTTRLG+YT L + P L +GMTAGA G+FV
 Sbjct: 100 VLAMYKGLSAAIMRQATYTTTTRLGVYTSLNDAKQKTNKTPNLLASMAMGMTAGAGISFV 159

Query: 137 GTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLRGCIPTMARAVVVNA 196
 G P+E+ LIRMTADGRLP D+RR Y FNAL RI REEGVL+LWRGC+PTM RA+VVNA
 Sbjct: 160 GNPSLILIRMTADGRLPVDERRNYTGFFNALFRIAREEGVLSLWRCVPTMGRAMVVNA 219

Query: 197 AQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGK 256
 AQLASYSQ+K +L+ S + I HF ASM SGL+TTAAS+PVDIAKTRIQNM++ G+
 Sbjct: 220 AQLASYSQAKAYLVSSQLLQEGIGLHFTASMFSGLITTAASLPVDIAKTRIQNMKVAPGE 279

Query: 257 -PEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMNKAYKR 309
 P YK+ +DV+ KV+R+EG F+LWKGF YY RLGPHTVLTFFI LEQ+N Y +
 Sbjct: 280 VPPYKSTVDVIVKIRHEGLFALWKGFATYYGRLGPHTVLTFFIILEQLNGLYNK 333

>gi|21358457|ref|NP_651703.1|  CG1907-PA [Drosophila melanogaster]
 gi|7301797|gb|AAF56907.1|  CG1907-PA [Drosophila melanogaster]
 gi|15292581|gb|AAK93559.1|  SD09259p [Drosophila melanogaster]
 Length = 317

Score = 348 bits (894), Expect = 8e-95

Identities = 177/299 (59%), Positives = 216/299 (72%), Gaps = 1/299 (0%)

Query: 15 KPRTSPKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKA 74
K + ++KFLFGGL+GMGAT+ VQPLDLVK RMQ+SG G+ +EY++S H + +I+
Sbjct: 11 KKAVATNAIKFLFGGLSGMGATMVVQPLDLVKTMRQISGAGSGKKEYRSSLHCIQTIVSK 70

Query: 75 EGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGA 134
EG +Y G+ A LLRQATYTT RLG+YT L + PG +G AGA GA
Sbjct: 71 EGPLALYQGIGAALLRQATYTTGRLGMYTYLNDLFREKFQSRSPGITDSMAMGTIAGACGA 130

Query: 135 FVGTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLRGCIPTMARAVVV 194
F+GTPAEVAL+RMT+DGRLP +RR Y NV NAL RITREEG+ LWRG +PT+ RA+VV
Sbjct: 131 FIGTPAEVALVRMTSDGRLPVAERRNYTNVANALARITREEGLTALWRGSLPTVGRAMVV 190

Query: 195 NAAQLASYSQSKQFLLD SGY-FSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMI 253
N QLASYSQ K + + I HFCASM+SGL+TT SMP+DIKTRIQN+M+
Sbjct: 191 NMTQLASYSQFKTYFRHGPLQMEEGIKLHFCASMLSGLLTTITSMPLDIAKTRIQNMMKV 250

Query: 254 DGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFFIFLEQMNKAYKRLFL 312
DGKPEY+ DVL +V R EG F+LWKGFTPYY RLGPHTVLTFFI LEQ+N+ Y + L
Sbjct: 251 DGKPEYRGTDVLLRVARQEGVFALWKGFTPYYCRLGPHTVLTFFIILEQLNQGYNKYVL 309

>gi|20151395|gb|AAM11057.1| **L** GH11346p [Drosophila melanogaster]
Length = 311

Score = 329 bits (843), Expect = 6e-89
Identities = 163/297 (54%), Positives = 212/297 (71%), Gaps = 3/297 (1%)

Query: 17 RTSPKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEG 76
+T P +KF+ GG +GM AT VQPLDL+K RMQ+SG TREYK SF L+ +LK EG
Sbjct: 10 KTVPTMFKFVMGGTSGMLATCIVQPLDLLKTRMQISGT-LGTREYKNSFEVLSKVLKNEG 68

Query: 77 LRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFV 136
+ +Y GLSAGLLRQATYT+ ++G+Y + + G P + +G+ AGA GA
Sbjct: 69 ILSLYNGLSAGLLRQATYTSKMGVYQMELDWYRKNFGNYPMSMVASMTMGIVAGAFGAMC 128

Query: 137 GTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLRGCIPTMARAVVVNA 196
G PAEVALIRM +D RL + RR YKNV +A +RI ++EGV+ LWRGC+PT+ RA+VVN
Sbjct: 129 GNPAEVALIRMMSDNRLIPEDRRNYKNVGDAFVRIVKDEGVVALWRGCLPTVGRAMVVNM 188

Query: 197 AQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGK 256
QLASYS K L GY S+ I H A+++SGL+T+ SMP+D+AKTRIQ M++IDGK
Sbjct: 189 VQLASYSMLKNQL--HGYLSEGIPLHLTAALVSGLLTSVTSMPPLDMAKTRIQMKVIDGK 246

Query: 257 PEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFFIFLEQMNKAYKRLFLS 313
PEY +DVL KV++ EG F++WKGFTPY R+GPHT+ +F+FLEQMNKAY + LS
Sbjct: 247 PEYSGTIDVLKKVLKNEGAFAVWKGFTPYLMRMGPHTIFSFFVLEQMNKAYSKHMLS 303

>gi|24657951|ref|NP_647924.2| **L** CG18418-PA [Drosophila melanogaster]
gi|7292530|gb|AAF47932.1| **L** CG18418-PA [Drosophila melanogaster]
Length = 311

Score = 329 bits (843), Expect = 6e-89
Identities = 163/297 (54%), Positives = 212/297 (71%), Gaps = 3/297 (1%)

Query: 17 RTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEG 76
 +T P +KF+ GG +GM AT VQPLDL+K RMQ+SG TREYK SF L+ +LK EG
 Sbjct: 10 KTVPTMFKFVMMGGTSGMLATCIVQPLDLLKTRMQISGT-LGTREYKNSFEVLKSVLKNEG 68

Query: 77 LRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFV 136
 + +Y GLSAGLLRQATYT+ ++G+Y + + G P + +G+ AGA GA
 Sbjct: 69 ILSLYNGLSAGLLRQATYTSKMGVYQMELDWYRKNFGNYPMSVASMTMGIVAGAFGAMC 128

Query: 137 GTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLRGCIPTMARAVVVNA 196
 G PAEVALIRM +D RL + RR YKNV +A +RI ++EGV+ LWRGC+PT+ RA+VVN
 Sbjct: 129 GNPAEVALIRMSDNRLMPEDRRNYKNVGDAFVRIVKDEGVVALWRGCLPTVGRAMVVNM 188

Query: 197 AQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNM RMIDGK 256
 QLASYS K L GY S+ I H A+++SGL+T+ SMP+D+AKTRIQ M++IDGK
 Sbjct: 189 VQLASYSLMKNQL--HGYLSEGIPLHLTAALVSGLLTSVTSMPPLDMAKTRIQMKVIDGK 246

Query: 257 PEYKNGLDVLFKVVRYE GFFSLWKGFPTPYARLGPHTVLTFFIFLEQMKNKAYKRLFLS 313
 PEY +DVL KV++ EG F++WKGFPTY R+GPHT+ +F+FLEQMKNKAY + LS
 Sbjct: 247 PEYSGTIDVLKKVLKNEGAFVWKGFPTPYLMRMGPHTIFS FVFLEQMKNKAYSKHMLS 303

>gi|24657945|ref|NP_647923.1| **L** CG7514-PA [Drosophila melanogaster]
 gi|7292529|gb|AAF47931.1| **L** CG7514-PA [Drosophila melanogaster]
 gi|19528119|gb|AAL90174.1| **L** AT25476p [Drosophila melanogaster]
 Length = 301

Score = 299 bits (766), Expect = 5e-80
 Identities = 161/296 (54%), Positives = 199/296 (67%), Gaps = 10/296 (3%)

Query: 17 RTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEG 76
 ++ P + ++ GGLAGM T VQPLDLVK RMQ+S A T EYK+SF L + K EG
 Sbjct: 8 KSIPGYMMYINGGLAGMLGTCIVQPLDLVKTRMQIS---ATTGEYKSSFDCLLKVKFNEG 64

Query: 77 LRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFV 136
 + +Y GLSAGL+RQATYTT R+G Y + + PP L +G+ AGA GA
 Sbjct: 65 ILALYNGLSAGLMRQATYTTARMGFYQMEIDAYRKQFNAPPTVLSMGMGILAGAFGAMF 124

Query: 137 GTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLRGCIPTMARAVVVNA 196
 G PAEVALIRM +D RLP +RR Y V NA +RI ++EGV+TLW+GC+PT+ RA++VN
 Sbjct: 125 GNPAEVALIRMSDNRLPPAERRNYTGVLNAFVRIVKDEGVITLWKGCMP TVGRAMIVNM 184

Query: 197 AQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNM RMIDGK 256
 QLASYSQ K S YFS + H A+M+SGL+TT ASMP+D+AKTRIQ +
 Sbjct: 185 VQLASYSQKAAF--SEYFS-GLSLHIAAAMMSGLLT TIASMPPLDMAKTRIQQK---T 237

Query: 257 PEYKNGLDVLFKVVRYE GFFSLWKGFPTPYARLGPHTVLTFFIFLEQMKNKAYKRLFL 312
 EYK +DVL KV + EG SLWKGFPTY RLGPH TV FIFLEQ+ KAYK + L
 Sbjct: 238 AEYKGTMDVLMKVSKNEGIASLWKGFPTPYLCRLGPHTVFAFIFLEQLTKAYKHIVL 293

>gi|48133286|ref|XP_393335.1| **L** similar to CG5076-PA [Apis mellifera]
 Length = 1871

Score = 238 bits (608), Expect = 1e-61
 Identities = 117/163 (71%), Positives = 132/163 (80%), Gaps = 2/163 (1%)

Query: 84 LSAGLLRQATYTTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFVGTAEVA 143

LSAGLLRQA+YTTTTRLG + L E ++ P FL+K +IG +AG GAFVGTPEVA
 Sbjct: 764 LSAGLLRQASYTTTTRLGTFEWLSELIS--KDRQPNFLMKLLIGSSAGCVGAFVGTPEVA 821

Query: 144 LIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARAVVVNAAQLASYS 203
 LIRMTADGRLP +RR YKN FNAL RI +EEG L LWRG +PTM RA+VVNAAQLASYS
 Sbjct: 822 LIRMTADGRLPLAERRNYKNAFNALFRIAKEEGFLALWRGTVPTMGRAMVVNAAQLASYS 881

Query: 204 QSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTR 246
 QSK+ LL++GYF DNIL HF +SMISGLVTT ASMPVDIAKTR
 Sbjct: 882 QSKETLLNTGYFEDNILLHFTSSMISGLVTTIASMPVDIAKTR 924

Score = 42.0 bits (97), Expect = 0.019
 Identities = 33/126 (26%), Positives = 47/126 (37%), Gaps = 2/126 (1%)

Query: 23 VKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEG--AKTREYKTSFHALTSILKAEGLRGI 80
 +K L G AG P ++ RM G A+ R YK +F+AL I K EG +
 Sbjct: 799 MKLLIGSSAGCVGAFVGTPEVALIRMTADGRLPLAERRNYKNAFNALFRIAKEEGFLAL 858

Query: 81 YTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGATGAFVGTPE 140
 + G + R +L Y+ E L LL M +G P
 Sbjct: 859 WRGTVPTMGRAMVVNAAQLASYSQSKETLLNTGYFEDNILLHFTSSMISGLVTTIASMPV 918

Query: 141 EVALIR 146
 ++A R
 Sbjct: 919 DIAKTR 924

Score = 40.4 bits (93), Expect = 0.049
 Identities = 21/73 (28%), Positives = 35/73 (47%), Gaps = 2/73 (2%)

Query: 218 NILCHFCASMISGLVTTAASMPVDIAKTRIQ-NMRM-IDGKPEYKNGLDVLFKVRYEGF 275
 N L +G V P ++A R+ + R+ + + YKN + LF++ + EGF
 Sbjct: 796 NFLMKLLIGSSAGCVGAFVGTPEVALIRMTADGRLPLAERRNYKNAFNALFRIAKEEGF 855

Query: 276 FSLWKGFTPYAR 288
 +LW+G P R
 Sbjct: 856 LALWRGTVPTMGR 868

>gi|2130090|pir||S65040 2-oxoglutarate/malate translocator (clones OMT134 and OMT1
 mitochondrial membrane - proso millet
 gi|1100739|dbj|BAA08103.1| 2-oxoglutarate/malate translocator [Panicum miliaceum]
 gi|1100741|dbj|BAA08104.1| 2-oxoglutarate/malate translocator [Panicum miliaceum]
 Length = 302

Score = 226 bits (577), Expect = 4e-58
 Identities = 137/290 (47%), Positives = 178/290 (61%), Gaps = 11/290 (3%)

Query: 25 FLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIYTGL 84
 F+ GG +GM AT +QP+D+VK ++QL GEG+ K +L EG+ Y GL
 Sbjct: 22 FVNGGASGMLATCVIQPIDMVKVKIQL-GECSAATVTK-----KMLANEGIGSFYKGL 73

Query: 85 SAGLLRQATYTTTTRLGIYTVLFERLTGA-DGTPPGFLLKAVIGMTAGATGAFVGTPEVA 143
 SAGLLRQATYTT RLG + VL + A +G P L KAVIG+TAGA GA VG+PA++A
 Sbjct: 74 SAGLLRQATYTTARLGSFRVLTNKAVEANEGKPLPLLQKAVIGLTAGAIGASVGSPADLA 133

Query: 144 LIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARAVVVNAAQLASYS 203
 LIRM AD LPA QRR YKN F+AL RI +EGVL LW+G PT+ RA+ +N LASY
 Sbjct: 134 LIRMQADSTLPAAQRRNYKNAFHALYRIVADEGVLLALWKGAGPTTVVRAMSLNMGLASYD 193

Query: 204 QSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRM-IDGKPEYKNG 262
 QS + D + + AS +SG +A S+P D KT+IQ M+ +GK Y
 Sbjct: 194 QSVELFRDK-LGAGELSTMLGASAVSGFCASACSLPFDYVKTQIQKMQPDANGKYPYTG 252

Query: 263 LDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTTFIFLEQMKNKAYKRLFL 312
 LD + K ++ G F + GF Y R+GPH +LT+IFL Q+ K K + L
 Sbjct: 253 LDCVMKTLKSGGPFKFYTGFPVYCVRIGPHVMLTWIFLNQIQKFEKDMGL 302

>gi|2130089|pir|S65042 2-oxoglutarate/malate translocator (clone OMT103), mitocho
 membrane - proso millet
 gi|1100743|dbj|BAA08105.1| 2-oxoglutarate/malate translocator [Panicum miliaceum]
 Length = 302

Score = 225 bits (573), Expect = 1e-57
 Identities = 139/300 (46%), Positives = 183/300 (61%), Gaps = 12/300 (4%)

Query: 16 PRTSPKSVK-FLFGGLAGMGATVFVQPLDLVKNMQLSGEGAKTREYKTSFHALTSILKA 74
 P + +VK F+ GG +GM AT +QP+D+VK ++QL GEG+ K +L
 Sbjct: 12 PSAAWMTVKPFVNGGASGMLATCVIQPIDMVVKIQL-GECSAATVTK-----KMLAN 63

Query: 75 EGLRGIYTGLSAGLLRQATYTTTTLGLIYTVLFRERLTGA-DGTPPGFLLKAVIGMTAGATG 133
 EG+ Y GLSAGLLRQATYTT RLG + VL + A +G P L KAVIG+TAGA G
 Sbjct: 64 EGIGSFYKGLSAGLLRQATYTTARLGSFRVLTNKAVEANEGKPLPLLQKAVIGLTAGAIG 123

Query: 134 AFVGTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARAVV 193
 A VG+PA++ALIRM AD LPA QRR YKN F+AL RI +EGVL LW+G PT+ RA+
 Sbjct: 124 ASVGSPADLALIRMQADSTLPAAQRRNYKNAFHALYRIVADEGVLLALWKGAGPTTVVRAMS 183

Query: 194 VNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRM- 252
 +N LASY QS + D+ + + AS +SG +A S+P D KT+IQ M+
 Sbjct: 184 LNMGLASYDQSVELFRDT-LGAGELSTMLGASAVSGFCASACSLPFDYVKTQIQKMQPD 242

Query: 253 IDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTTFIFLEQMKNKAYKRLFL 312
 +GK Y LD + K ++ G F + GF Y R+ PH +LT+IFL Q+ K K + L
 Sbjct: 243 ANGKYPYTGSLDCVMKTLKSGGPFKFYTGFPVYCVRIAPHVMLTWIFLNQIQKFEKDIGL 302

>gi|23489162|gb|EAA21506.1| putative oxoglutarate/malate translocator protein [Pla
 yoelii yoelii]
 Length = 319

Score = 224 bits (571), Expect = 2e-57
 Identities = 115/288 (39%), Positives = 172/288 (59%), Gaps = 7/288 (2%)

Query: 25 FLFGGLAGMGATVFVQPLDLVKNMQLSGEGAKTREYKTSFHALTSILKA EGLRGIYTGL 84
 F GG++GM AT +QPLD+VK R+QL+ EG K F +I+K EG+ +Y GL
 Sbjct: 37 FCIGGMSGMFATFCIQPLDMVKVRIQLNAEGKNA--IKNPFIKNIIDEGVLSLYKGL 94

Query: 85 SAGLLRQATYTTTTLGLIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFVGTPEAVAL 144
 AGL RQ YTT RLG++ F + +G P F K V + AG GAF+G PA+++L
 Sbjct: 95 DAGLTRQVIYTTGRLGLFRT-FSDIVKNEGEPLPFYKKCVCALAAGGIGAFLGNPADLSL 153

Query: 145 IRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARAVVVNAAQLASYSQ 204

IR+ AD LP + +R Y VFNA+ RIT+EEG+ +LW+G +PT+ARA+ +N L++Y Q
 Sbjct: 154 IRLQADNTLPKELKRNYTGVFNAIYRITKEEGICSLWKGSVPTIARAMSLNLGMLSTYDQ 213
 Query: 205 SKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRM--IDGKPEYKNG 262
 SK++L Y + + AS+ISG S+P D KT +Q M++ + K YKN
 Sbjct: 214 SKEYL--EKYLGVMKTNLVASVISGFFAVTMSLPDFVKTCTMQKMKVDPVTNKMPYKNM 271
 Query: 263 LDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMKNKAYKRL 310
 LD +K+ + G + + YY R+ PH ++T + ++ +N +K +
 Sbjct: 272 LDGSYKLYKKGGISIFYASYGTYYVRIAPHAMITLVTMDYLNLFKHI 319

>gi|37964368|gb|AAR06239.1| dicarboxylate/tricarboxylate carrier [Citrus junos]
 Length = 299

Score = 224 bits (571), Expect = 2e-57
 Identities = 137/307 (44%), Positives = 184/307 (59%), Gaps = 14/307 (4%)

Query: 11 GIDGKPRTS---PKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHA 67
 G + KP+++ P F+ GG +GM AT +QP+D++K R+QL G+G+ KT
 Sbjct: 2 GEEKKPQSAGVWPTVKPFVNGGASGMLATCVIQPIDMIKVRIQL-GQGSAGTVTKT---- 56
 Query: 68 LTSILKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFERLTGA-DGTPPGFLLKAVIG 126
 +LK EG Y GLSAGLLRQATYTT RLG + +L + A DG P KA+ G
 Sbjct: 57 ---MLKNEGFGAFYKGLSAGLLRQATYTTARLGSFRILTNTKAIEANDGKPLPLYQKALCG 113
 Query: 127 MTAGATGAFVGTAEVALIRMADGRLPADQRRGYKNVFNALIRITREEGVTLWRGCIIP 186
 +TAGA GA VG+PA++ALIRM AD LPA QRR Y N F AL RI +EGVL LW+G P
 Sbjct: 114 LTAGAIGASVSPADLALIRMQADATLPAAQRRHYTNAFQALYRIVTDEGVLLALWKAGAP 173
 Query: 187 TMAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTR 246
 T+ RA+ +N LAS Y QS +F D+ S+ + AS +SG +A S+P D KT+
 Sbjct: 174 TVVRAMALNMGLASYDQSVEFFRDACGLSE-LPTVIGASTVSGFFASACSLPFDYVKTQ 232
 Query: 247 IQNMRM-IDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMKN 305
 IQ M+ GK Y +D K ++ G F + GF Y R+ PH ++T+IFL Q+ K
 Sbjct: 233 IQKMQPD AQGKYPYTGSMDCAMKTLKAGGPFKPYTGFPVYCVRIAPHVMMTWIFLNQIQK 292
 Query: 306 AYKRLFL 312
 K++ L
 Sbjct: 293 LEKKVGL 299

>gi|15241167|ref|NP_197477.1| dicarboxylate/tricarboxylate carrier (DTC) [Arabidop
 gi|13430482|gb|AAK25863.1| putative oxoglutarate/malate translocator protein [Ara
 thaliana]
 gi|15810537|gb|AAL07156.1| putative oxoglutarate/malate translocator protein [Ara
 thaliana]
 gi|19913113|emb|CAC84549.1| dicarboxylate/tricarboxylate carrier [Arabidopsis tha
 gi|21554032|gb|AAM63113.1| oxoglutarate/malate translocator-like protein [Arabido
 thaliana]
 Length = 298

Score = 224 bits (570), Expect = 3e-57
 Identities = 129/288 (44%), Positives = 177/288 (61%), Gaps = 11/288 (3%)

Query: 25 FLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIYTGL 84
 F+ GG +GM AT +QP+D++K R+QL G+G+ T++LK EG+ Y GL

Sbjct: 18 FVNGGASGMLATCVIQPIDMIKVRIQL-GQGSAA-----ITTNMLKNEGVGAFYKGL 69

Query: 85 SAGLLRQATYTTTRLGIYTVLFR-LTGADGTPPGFLLKAVIGMTAGATGAFVGTAEVA 143
SAGLLRQATYTT RLG + +L + + DG P KA+ G+TAGA GA VG+PA++A

Sbjct: 70 SAGLLRQATYTTARLGSFKLLTAKAIESNDGKPLPLYQKALCGLTAGAIGACVGPADLA 129

Query: 144 LIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRCIPTMARAVVVNAAQLASYS 203
LIRM AD LP QRR Y N F+AL RI+ +EGVL LW+GC PT+ RA+ +N LAS Y

Sbjct: 130 LIRMQADNTLPLAQRRNYTNAFHALTRISADEGVLLALWKGCGPTVVRAMALNMGMMLASYD 189

Query: 204 QSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRM-IDGKPEYKNG 262
QS +++ D+ F + + AS +SG A S+P D KT+IQ M+ GK Y

Sbjct: 190 QSAEYMRDNLGFGE-MSTVVGASAVSGFCAAACSLPFDVKTQIQKMOPDAQGKYPYTG 248

Query: 263 LDVLFKVVR YEGFFSLWKGFTPPYARLGPHTVLT FIFLEQMKNKAYKRL 310
LD K ++ G + GF Y R+ PH ++T+IFL Q+ K K++

Sbjct: 249 LDCAMKTLKEGGPLKFYSGFPVYCVRIAPHVMMTWIFLNQITKFQKKI 296

>gi|19913107|emb|CAC84546.1| dicarboxylate/tricarboxylate carrier [Nicotiana tabac
Length = 295

Score = 221 bits (563), Expect = 2e-56
Identities = 135/303 (44%), Positives = 179/303 (59%), Gaps = 14/303 (4%)

Query: 15 KPRTS---PKSVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI 71
KP++ P F+ GG +GM AT +QP+D++K R+QL G+G+ KT +

Sbjct: 2 KPKSGGVWPTVKPFVNGGASGMLATCVIQPIDMIKVRIQL-GQGSADVTKT-----M 53

Query: 72 LKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFR-LTGA-DGTPPGFLLKAVIGMTAG 130
LK EG Y GLSAGLLRQATYTT RLG + +L + A +G P KA+ G+TAG

Sbjct: 54 LKNEGFAGFYKGLSAGLLRQATYTTARLGSFRILTNAIEANEGKPLPLYQKALCGLTAG 113

Query: 131 ATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRCIPTMAR 190
A GA G+PA++ALIRM AD LP QRR Y N F+AL RI +EGVL LW+G PT+ R

Sbjct: 114 AIGACFGSPADLALIRMQADATLPLAQRRHYTNAFHALSRIVADEGVLLALWKGAGPTVVR 173

Query: 191 AVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNM 250
A+ +N LAS Y QS +F D+ S+ AS +SG A S+P D KT+IQ M

Sbjct: 174 AMALNMGMMLASYDQSVEFCRDNLGMSEAATV-VGASSVSGFFAAACSLPFDYVKTQIQKM 232

Query: 251 RM-IDGKPEYKNGLDVLFKVVR YEGFFSLWKGFTPPYARLGPHTVLT FIFLEQMKNKAYKR 309
+ +GK Y D K ++ G F + GF Y R+ PH ++T+IFL Q+ KA K+

Sbjct: 233 QPDAEGKLPYSGSFD CAMKTLKAGGPFKFYTGFVYCVRIAPHVMMTWIFLNQIQKAEKK 292

Query: 310 LFL 312
L L

Sbjct: 293 LGL 295

>gi|10798640|emb|CAC12820.1| mitochondrial 2-oxoglutarate/malate carrier protein [t
tabacum]
Length = 297

Score = 221 bits (563), Expect = 2e-56
Identities = 135/303 (44%), Positives = 179/303 (59%), Gaps = 14/303 (4%)

Query: 15 KPRTS---PKSVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI 71

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      KP++      P      F+ GG +GM AT  +QP+D++K R+QL G+G+      KT      +
Sbjct: 4      KPKSGGVWPTVKPFVNGGASGMLATCVIQPIDMIKVRIQL-GQGSADVDTKT-----M 55

Query: 72      LKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGA-DGTPPGFLLKAVIGMTAG 130
      LK EG      Y GLSAGLLRQATYTT RLG + +L +      A +G P      KA+ G+TAG
Sbjct: 56      LKNEGFAGFYKGLSAGLLRQATYTTARLGSFRILTNTKAIEANEGKPLPLYQKALCGLTAG 115

Query: 131     ATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMAR 190
      A GA      G+PA++ALIRM AD  LP  QRR Y N F+AL RI  +EGVL LW+G  PT+ R
Sbjct: 116     AIGACFGSPADLALIRMQADATLPLAQRRHYTNAFHALSRIVADEGVLLWKGAGPTVVR 175

Query: 191     AVVVNAAQLASYSQSKQFLDLSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNM 250
      A+ +N      LASYS QS +F  D+   S+           AS +SG      A S+P D  KT+IQ M
Sbjct: 176     AMALNMGMLASYDQSVEFCRDNLGMSEAATV-VGASSVSGFFAAACSLPFDYVKTQIQKM 234

Query: 251     RM-IDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMNKAYKR 309
      +  +GK Y      D  K ++  G F  + GF  Y  R+ PH ++T+IFL Q+ KA K+
Sbjct: 235     QPDAEGKLPYSGSFDCAKMTLKGAGPFFKYTGFPVYCVRIAPHVMMTWIFLNQIQKAEKK 294

Query: 310     LFL 312
      L L
Sbjct: 295     LGL 297

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>gi|19913105|emb|CAC84545.1| dicarboxylate/tricarboxylate carrier [Nicotiana tabac
Length = 297

Score = 220 bits (561), Expect = 3e-56
Identities = 136/303 (44%), Positives = 179/303 (59%), Gaps = 14/303 (4%)

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Query: 15      KPRTS---PKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSI 71
      KP++      P      F+ GG +GM AT  +QP+D++K R+QL G+G+      KT      +
Sbjct: 4      KPKSGGVWPTVKPFVNGGASGMLATCVIQPIDMIKVRIQL-GQGSADVDTKT-----M 55

Query: 72      LKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGA-DGTPPGFLLKAVIGMTAG 130
      LK EG      Y GLSAGLLRQATYTT RLG +  L  +      A +G P      KA+ G+TAG
Sbjct: 56      LKNEGFAGFYKGLSAGLLRQATYTTARLGSFRSLTNKAIEANEGKPLPLYQKALCGLTAG 115

Query: 131     ATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMAR 190
      A GA VG+PA++ALIRM AD  LP  QRR Y N F+AL RI  +EGVL LW+G  PT+ R
Sbjct: 116     AIGACVGSADLALIRMQADATLPLAQRRHYTNAFHALSRIVADEGVLLWKGAGPTVVR 175

Query: 191     AVVVNAAQLASYSQSKQFLDLSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNM 250
      A+ +N      LASYS QS +F  D+   S+           AS +SG      A S+P D  KT+IQ M
Sbjct: 176     AMALNMGMLASYDQSVEFCRDNLGMSEAATV-VGASSVSGFFAAACSLPFDYVKTQIQKM 234

Query: 251     RM-IDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMNKAYKR 309
      +  +GK Y      D  K ++  G F  + GF  Y  R+ PH ++T+IFL Q+ KA K+
Sbjct: 235     QPDAEGKLPYSGSFDCAKMTLKGAGPFFKYTGFPVYCVRIAPHVMMTWIFLNQIQKAEKK 294

Query: 310     LFL 312
      L L
Sbjct: 295     LGL 297

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>gi|7489246|pir||T07405 oxoglutarate/malate translocator - potato
gi|1486472|emb|CAA68164.1| oxoglutarate malate translocator [Solanum tuberosum]
Length = 297

Score = 217 bits (553), Expect = 2e-55
Identities = 131/295 (44%), Positives = 175/295 (59%), Gaps = 11/295 (3%)

Query: 20 PKSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRG 79
P F+ GG++GM AT +QP+D++K R+QL G+G+ KT +LK EG
Sbjct: 12 PTVKPFINGGVSGMLATCVIQPIDMIKVRIQL-GQGSAADVTKT-----MLKNEGFGA 63

Query: 80 IYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGA-DGTPPGFLLKAVIGMTAGATGAFVGT 138
Y GLSAGLLRQATYTT RLG + +L + A +G P KA+ G+TAGA GA VG+
Sbjct: 64 FYKGLSAGLLRQATYTTARLGSFRILTINKAIEANEGKPLPLYQKALCGLTAGAIGATVGS 123

Query: 139 PAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWRCIPTMARAVVVNAAQ 198
PA++ALIRM AD LP QRR Y N F+AL RI +EGVL LW+G PT+ RA+ +N
Sbjct: 124 PADLALIRMQADATLPLAQRRNYTNAFHALSRIAVIDEGVLALWKGAGPTVVRAMALNMGM 183

Query: 199 LASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRM-IDGKP 257
LAS Y QS +F D+ + AS +SG A S+P D KT+IQ M+ +GK
Sbjct: 184 LASYDQSVEFFRDNLGMGEAATV-VGASSVSGFFAAACSLPFDYVKTQIQKMOPDAEGKL 242

Query: 258 EYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMNKAYKRLFL 312
Y D K ++ G F + GF Y R+ PH ++T+IFL Q+ K K++ L
Sbjct: 243 PYTGSFDCAMKTLKAGGPFKFYTGFPVYCIPIAPHVMMTWIFLNQIQKVEKKIGL 297

>gi|19913109|emb|CAC84547.1| dicarboxylate/tricarboxylate carrier [Nicotiana tabac
Length = 300

Score = 217 bits (552), Expect = 3e-55
Identities = 137/312 (43%), Positives = 180/312 (57%), Gaps = 20/312 (6%)

Query: 3 ATASAGAGGIDGKPRTPSPSVKFLFGGLAGMGATVVFVQPLDLVKNRMQLSGEGAKTREYK 62
+T+SAGA P P F GG +GM AT +QP+D++K R+QL G+G+ +
Sbjct: 7 STSSAGAW-----PTVKP----FANGGASGMLATCVIQPIDMIKVRIQL-GQGSAGEVTR 56

Query: 63 TSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVLFRERLTGA-DGTPPGFLL 121
T +LK EG Y GLSAGLLRQATYTT RLG + VL + A DG P
Sbjct: 57 T-----MLKNEGFGAFYKGLSAGLLRQATYTTARLGSFRVLTNKAIEANDGKPLPLYQ 109

Query: 122 KAVIGMTAGATGAFVGTTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTW 181
KA+ G+TAGA GA G+PA++ALIRM AD LP QRR Y N F+AL RI +EGVL+LW
Sbjct: 110 KALCGLTAGAIGACFGSPADLALIRMQADATLPVAQRRNYTNAFHALYRIVADEGVLSLW 169

Query: 182 RGCIPMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVD 241
+G PT+ RA+ +N LAS Y QS +F D+ + AS +SG A S+P D
Sbjct: 170 KGAGPTVVRAMALNMGMLASYDQSVEFFKDNLGMGEAATV-VGASSVSGFFAAACSLPFD 228

Query: 242 IAKTRIQNMRM-IDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFL 300
KT+IQ M+ GK Y D K ++ G F + GF Y R+ PH ++T+IFL
Sbjct: 229 YVKTQIQKMOPDAQGKYPYTGSFDCAMKTLKSGGPFKFYTGFPVYCVRIAPHVMMTWIFL 288

Query: 301 EQMNKAYKRLFL 312
Q+ K K++ L
Sbjct: 289 NQIQKVEKKIGL 300

>gi|23612776|ref|NP_704315.1| oxoglutarate/malate translocator protein, putative [falciparum 3D7]

gi|23499054|emb|CAD51134.1| oxoglutarate/malate translocator protein, putative [P
falciparum 3D7]
Length = 318

Score = 215 bits (547), Expect = 1e-54
Identities = 114/288 (39%), Positives = 165/288 (57%), Gaps = 7/288 (2%)

Query: 25 FLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIYTGL 84
F GG +GM AT +QPLD+VK R+QL+ EG + F I+K EG +Y GL
Sbjct: 35 FAVGGASGMFATFCIQPLDMVKVRIQLNAEGKNV--LRNPFIVAKDIIKNEGFLSLYKGL 92

Query: 85 SAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGATGAFVGTAEVAL 144
AGL RQ YTT RLG++ F + +G P F K + AG GAF+G PA+++L
Sbjct: 93 DAGLTRQVIYTTGRLGLFRT-FSDMVKKEGEPLPFYKKCFCALAAGGLGAFIGNPADLSL 151

Query: 145 IRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLGCIPTMARAVVVNAAQLASYSQ 204
IR+ AD LP + +R Y VFNAL RI++EEG+ LW+G +PT+ARA+ +N L++Y Q
Sbjct: 152 IRLQADNTLPKELKRNYTG VFNALYRISKEEGLFALWKGSVPTIARAMSLNLGMLSTYDQ 211

Query: 205 SKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRM--IDGKPEYKNG 262
SK+FL Y + + AS+ISG S+P D KT +Q M+ + K YKN
Sbjct: 212 SKEFL--QKYLGVGMKTNLVASVISGFFAVTSLPFDVFKTCMQMKADPVTCKMPYKMN 269

Query: 263 LDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMNKAYKRL 310
LD ++ + G + + YY R+ PH ++T I ++ +N K++
Sbjct: 270 LDCSIQLYKKGGISIFYSSYATYYVRIAPHAMITLITVDYLNLLKKI 317

>gi|38101905|gb|EAA48805.1| hypothetical protein MG00463.4 [Magnaporthe grisea 70-
Length = 1536

Score = 213 bits (543), Expect = 4e-54
Identities = 114/278 (41%), Positives = 161/278 (57%), Gaps = 5/278 (1%)

Query: 22 SVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIY 81
++ FL GG AGM AT +QP+D++K R+QL+GEG T IL + +Y
Sbjct: 47 ALPFLNGGAAGMVATTVIQPVDMIKVRLQLAGEGMAGGVKPTPLSVTRDILASGRALDLY 106

Query: 82 TGLSAGLLRQATYTTTTRLGIYTVLFERLTGA---DGTPPGFLLKAVIGMTAGATGAFVGT 138
TGLSAGLLRQA YTT RLG + LT +G+ GF +A G++AG A +G
Sbjct: 107 TGLSAGLLRQAVYTTARLGFFDTFMGTLTAKAKENGSAIGFKERAAAGLSAGGLAAMIGN 166

Query: 139 PAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLGCIPTMARAVVVNAAQ 198
PA++ALIRM +DG P + R+ YK+V +AL RIT+ EG+ LW G PT+ RA+ +N Q
Sbjct: 167 PADLALIRMQSDGLKPESRQNYKSVIDALARITKNEGIAALWSGATPTTVVRAMALNFGQ 226

Query: 199 LASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQ-NMRMIDGKP 257
LA +S++K L + + AS ++G + S+P D KTR+Q R DGK
Sbjct: 227 LAFFSEAKAQLKSRTDLNPRVQT-LTASAVAGFFASFFSLPFDVFKTRLQKQQRGPDGKL 285

Query: 258 EYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVL 295
Y+N +D +V + EG ++GF YY R+ PH +L
Sbjct: 286 PYRNMIDCFGQVAKQEGALRFYRGFWTYVRIAPHALL 323

>gi|15227225|ref|NP_179836.1| mitochondrial substrate carrier family protein [Arab
thaliana]
gi|25295876|pir||D84613 hypothetical protein At2g22500 [imported] - Arabidopsis t

gi|4544443|gb|AAD22351.1| putative mitochondrial dicarboxylate carrier protein [A
thaliana]
gi|13877659|gb|AAK43907.1| putative mitochondrial dicarboxylate carrier protein [A
thaliana]
gi|23297154|gb|AAN13106.1| putative mitochondrial dicarboxylate carrier protein [A
thaliana]
Length = 313

Score = 209 bits (532), Expect = 6e-53
Identities = 123/304 (40%), Positives = 180/304 (59%), Gaps = 20/304 (6%)

Query: 25 FLFGGLAGMGATVFVQPLDLVKNRMQSLGEGAKTR-----EYKTSFHAL----- 68
F GG+A + A PLDL+K RMQ L GE A + + T+ +A
Sbjct: 6 FAEGGIASIVAGCSTHPLDLIKVRMQLGESAPIQTNLRLPALAFQTSTTVNAPPLRVGVI 65

Query: 69 ---TSILKAEGLRGIYTGLSAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPPGFLLKAVI 125
+ +++ EG+R +++G+SA +LRQ Y+TTR+G+Y ++ T + + K
Sbjct: 66 GVGSRLIREEGMRALFSGVSATVLRQTLYSTTRMGLYDIKGEWTDPETKTMPLMKKIGA 125

Query: 126 GMTAGATGAFVGTPEAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWLRGCI 185
G AGA GA VG PA+VA++RM ADGRLP RR YK+V +A+ ++ R EGV +LWRG
Sbjct: 126 GAIAGAIGAAGVGNPADVAMVRMQADGRLPLTDRRNYKSVLDAITQMIRGEGVTSLWRGSS 185

Query: 186 PTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKT 245
T+ RA++V ++QLASY K+ +L+ G D + H AS +G V + AS PVD+ KT
Sbjct: 186 LTINRAMLVTS SQLASYDSVKETILEKGLLDGLGTHVSASFAAGFVASVASNPVDVIKT 245

Query: 246 RIQNM RMIDG-KPEYKNGLDVLFKVVR YEGFFSLWKGFTPYYARLGPHTVLT FIFLEQMN 304
R+ NM+++ G P YK +D K V+ EG SL+KGF P +R P TV+ F+ LEQ+
Sbjct: 246 RVMNMKV VAGVAPPYKGA VDCALKT VKAEGIMSLYKGF IPTVSRQAPFTV VLFVLTLEQVK 305

Query: 305 KAYK 308
K +K
Sbjct: 306 KLFK 309

Score = 57.8 bits (138), Expect = 3e-07
Identities = 41/173 (23%), Positives = 75/173 (43%), Gaps = 3/173 (1%)

Query: 41 PLDLVKNRMQSLGEGAKT--REYKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTR 98
P D+ RMQ G T R YK+ A+T +++ EG+ ++ G S + R T+++
Sbjct: 139 PADVAMVRMQADGRLPLTDRRNYKSVLDAITQMIRGEGVTSLWRGSSLTINRAMLVTSQ 198

Query: 99 LGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFVGTPEAEVALIRMTADGRLPADQR 158
L Y + E + G AG + P +V R+ + ++ A
Sbjct: 199 LASYDSVKETILEKGLLDGLGTHVSASFAAGFVASVASNPVDVIKTRVM-NMKVVAGVA 257

Query: 159 RGYKNVFNALIRITREEGVTLWLRGCIPTMARAVVVNAAQLASYSQSKQFLLD 211
YK + ++ + EG+++L++G IPT++R + Q K+ D
Sbjct: 258 PPYKGA VDCALKT VKAEGIMSLYKGF IPTVSRQAPFTV VLFVLTLEQVKKLFKD 310

>gi|49097862|ref|XP_410391.1| hypothetical protein AN6254.2 [Aspergillus nidulans
gi|40739448|gb|EAA58638.1| hypothetical protein AN6254.2 [Aspergillus nidulans FG
Length = 308

Score = 206 bits (525), Expect = 4e-52
Identities = 121/288 (42%), Positives = 163/288 (56%), Gaps = 11/288 (3%)

Query: 25 FLFGGLAGMGATVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIYTGL 84
 F FGG A A PLDLVK R+Q G GA + T H IL+ G G+Y GL
 Sbjct: 27 FWFSGSASCFAAAVTHPLDLVKVRLQTRGPGAPSTMLGTFGH---ILRNNGFFGLYNGL 82

Query: 85 SAGLLRQATYTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGM--TAGATGAFVGTPEV 142
 SA LLRQ TY+TTR GIY L R T +P F L +GM T+G G G PA+V
 Sbjct: 83 SAALLRQLTYSTTRFGIYEELKSRTSPSQSPSFFTL---LGMACTSGILGGIAGNPADV 139

Query: 143 ALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCIPTMARAVVVNAAQLASY 202
 +RM +D LP QRR Y++ F+ L+++TR EG +L+RG P RAV++ ++QL SY
 Sbjct: 140 LNVRMQSDAALPPAQRRNYRHAFHGLVQMTRTEGFSSLFGRVWPNSTRAVLMTSSQLVSY 199

Query: 203 SQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGKPEYKNG 262
 K+ L+ DN++ HF AS +G V T PVD+ KTR+ M + N
 Sbjct: 200 DVFKRLCLEKFGMKDNVTHFSASFAAGFVATTVCSPVDVIKTRV--MSASPSETRGHNI 257

Query: 263 LDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTTFIFLEQMNKAYKRL 310
 + +L ++ R EG ++G+ P + RLGPHT+ TFIFLE+ K Y+ L
 Sbjct: 258 VGLLREISRKEGLAWAFRGWVPSFIRLGPHTIATFIFLEEKKLYRYL 305

>gi|21554157|gb|AAM63236.1| putative mitochondrial dicarboxylate carrier protein [thaliana]
 Length = 313

Score = 206 bits (523), Expect = 7e-52
 Identities = 123/304 (40%), Positives = 178/304 (58%), Gaps = 20/304 (6%)

Query: 25 FLFGGLAGMGATVQPLDLVKNRMQLSGEGAKTR-----EYKTSFHAL----- 68
 F GG+A + A PLDL+K RMQL GE A + + T+ +A
 Sbjct: 6 FAEGGIASIVAGCSTHPLDLIKVRMQLQGESAPIQTNLRLPALAFQTSTTVNAPPLRVGVI 65

Query: 69 ---TSILKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFRERLTGADGTPPGFLLKAVI 125
 + +++ EG+R +++G+SA +LRQ Y+TTR+G+Y ++ T + K
 Sbjct: 66 GVGSRLIREEGMRALFSGVSATVLRQTLYSTTRMGLYDIKGEWTDPGTKTMPLMKKIGA 125

Query: 126 GMTAGATGAFVGTPEAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTTLWRGCI 185
 G AGA GA VG PA+VA++RM ADGRLP RR YK+V +A+ ++ R EGV +LWRG
 Sbjct: 126 GAIAGAIGAAGVNPADVAMVRMQADGRLPLTDRRNYKSVLDAITQMIRGEGVTSLSWRGSS 185

Query: 186 PTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKT 245
 T+ RA++V ++QLASY K+ +L+ G D + H AS +G V + AS PVD+ KT
 Sbjct: 186 LTINRAMLVTSQSLASYDSVKETILEKGLLDGLGTHVLASFAAGFVASVASNPVDVIKT 245

Query: 246 RIQNMRMIDG-KPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTTFIFLEQMN 304
 R+ NM+++ G P YK +D K V+ EG SL+KGF P +R P TV+ F+ LEQ+
 Sbjct: 246 RVMNMKVAVGAPPYKGAVDCALKTVKAEGIMSLYKGFIPVSRQAPFTTVLVFTLEQVK 305

Query: 305 KAYK 308
 K K
 Sbjct: 306 KLLK 309

Score = 59.7 bits (143), Expect = 8e-08
 Identities = 42/173 (24%), Positives = 77/173 (44%), Gaps = 3/173 (1%)

Query: 41 PLDLVKNRMQLSGEGAKT--REYKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTR 98

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      P D+  RMQ  G    T  R YK+  A+T +++ EG+  ++ G S  + R    T+++
Sbjct: 139 PADVAMVRMQADGRLPLTDRRNYKSVLDAITQMIRGEGVTSLWRGSSLTINRAMLVTSQ 198

Query: 99  LGIYTVLFERLTGADGTPPGFLLKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQR 158
      L  Y  + E  +          G    +  AG    +  P +V  R+  + ++ A
Sbjct: 199 LASYDSVKETILEKGLLKDGLGTHVLASFAAGFVASVASNPVDVIKTRVM-NMKVVAGVA 257

Query: 159 RGYKNVFNALIRITREEGVLTLRGCIPTMARAVVVNAAQLASYSQSKQFLLD 211
      YK    +  ++  + EG+++L++G IPT++R          +  Q K+ L D
Sbjct: 258 PPYKGAVDCALKTVKAEGIMSLYKGFIP TVSRQAPFTVVLFVTLEQVKKLLKD 310

```

>gi|13878155|gb|AAK44155.1| putative mitochondrial dicarboxylate carrier protein [thaliana]
Length = 313

Score = 205 bits (521), Expect = 1e-51
Identities = 122/304 (40%), Positives = 179/304 (58%), Gaps = 20/304 (6%)

```

Query: 25  FLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTR-----EYKTSFHAL----- 68
      F  GG+A + A      PLDL+K RML GE A  +          +  T+ +A
Sbjct: 6   FAEGGIASIVAGCSTHPLDLIKVRMQLGESAPIQTNLRLPALAFQTSTTVNAPPLRVGVI 65

Query: 69  ---TSILKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFERLTGADGTPPGFLLKAVI 125
      + +++ EG+R +++G+SA +LRQ  Y+TTR+G+Y ++      T  +          + K
Sbjct: 66  GVGSRLIREEGMRALFSGVSATVLRQTLYSTTRMGLYDIKGEWTDPETKTMLMKKIGA 125

Query: 126 GMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTLRGCI 185
      G  A A GA VG PA+VA++RM ADGRLP  RR YK+V +A+ ++ R EGV +LWRG
Sbjct: 126 GAIAVAIGA AVGNPADVAMVRMQADGRLPLTDRRNYKSVLDAITQMIRGEGVTSLWRGSS 185

Query: 186 PTMARAVVVNAAQLASYSQSKQFLDSDGYFSDNILCHFCASMISGLVTTAASMPVDIAKT 245
      T+ RA++V ++QLASY  K+ +L+ G  D +  H AS  +G V + AS PVD+ KT
Sbjct: 186 LTINRAMLVTSQQLASYDSVKETILEKGLLKDGLGTHVSASFAAGFVASVASNPVDVIKT 245

Query: 246 RIQNM RMIDG-KPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFLEQMN 304
      R+ NM+++ G  P YK  +D  K V+ EG  SL+KGF P  +R  P TV+ F+ LEQ+
Sbjct: 246 RVMNMKV VAGVAPPYKGAVDCALKTVKAEGIMSLYKGFIP TVSRQAPFTVVLFVTLEQVK 305

Query: 305 KAYK 308
      K +K
Sbjct: 306 KLFK 309

```

Score = 58.5 bits (140), Expect = 2e-07
Identities = 47/201 (23%), Positives = 84/201 (41%), Gaps = 3/201 (1%)

```

Query: 13  DGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKT--REYKTSFHALTS 70
      D + +T P  K  G +A          P D+  RMQ  G    T  R YK+  A+T
Sbjct: 111 DPETKTMLMKKIGAGAI A VAIGA AVGNPADVAMVRMQADGRLPLTDRRNYKSVLDAITQ 170

Query: 71  ILKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAG 130
      +++ EG+  ++ G S  + R    T+++L  Y  + E  +          G          AG
Sbjct: 171 MIRGEGVTSLWRGSSLTINRAMLVTSQQLASYDSVKETILEKGLLKDGLGTHVSASFAAG 230

Query: 131 ATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTLRGCIPTMAR 190
      +  P +V  R+  + ++ A    YK    +  ++  + EG+++L++G IPT++R
Sbjct: 231 FVASVASNPVDVIKTRVM-NMKVVAGVAPPYKGAVDCALKTVKAEGIMSLYKGFIP TVSR 289

```


Query: 191 AVVVNAAQLASYSQSKQFLLD 211
+ Q K+ D
Sbjct: 290 QAPFTVVLFTLEQVKKLFKD 310

>gi|15233884|ref|NP_194188.1| mitochondrial substrate carrier family protein [Arab
thaliana]
gi|7488415|pir|T05577 uncoupling protein homolog F22K18.230 - Arabidopsis thalia
gi|4220533|emb|CAA23006.1| putative mitochondrial uncoupling protein [Arabidopsis
gi|7269307|emb|CAB79367.1| putative mitochondrial uncoupling protein [Arabidopsis
gi|14596143|gb|AAK68799.1| putative mitochondrial uncoupling protein [Arabidopsis
gi|21537077|gb|AAM61418.1| putative mitochondrial uncoupling protein [Arabidopsis
gi|30984524|gb|AAP42725.1| At4g24570 [Arabidopsis thaliana]
Length = 313

Score = 204 bits (519), Expect = 2e-51
Identities = 124/307 (40%), Positives = 171/307 (55%), Gaps = 30/307 (9%)

Query: 25 FLFGGLAGMGATVFVQPLDLVKNRMLSGEGAKT-----REYKTSFHALTS- 70
F+ GG+A + A PLDL+K R+QL GE T +F TS
Sbjct: 6 FVEGGIASVIAGCSTHPLDLIKVRLQLHGEAPSTTTVTLLRPALAFPNSSPAAFLETTSS 65

Query: 71 -----ILKAEGLRGIYTGLSAGLLRQATYTTTTLRGLIYTVLFRERLTGADGTTPPG 118
I+K+EG +++G+SA LLRQ Y+TTR+G+Y VL + T +
Sbjct: 66 VPKVGPISLGINIVKSEGAAALFSGVSATLLRQTLYSTTRMGLYEVLKNKWTDPESGKLN 125

Query: 119 FLLKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGV 178
K G+ AG GA VG PA+VA++RM ADGRLP QRR Y V +A+ + + EGV
Sbjct: 126 LSRKIGAGLVAGGIGAAGVNPADVAMVRMQADGRLPLAQRRNYAGVGDAIRSMVKGEV 185

Query: 179 TLWRGCIPTMARAVVVNAAQLASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASM 238
+LWRG T+ RA++V AAQLASY Q K+ +L++G +D + H AS +G V + AS
Sbjct: 186 SLWRGSALTINRAMIVTAAQLASYDQFKEGILENGVMNDGLGTHVVASFAAGFVASVASN 245

Query: 239 PVDIAKTRIQNMRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFI 298
PVD+ KTR+ NM++ Y D K V+ EG +L+KGF P R GP TV+ F+
Sbjct: 246 PVDVIKTRVMNMKV---GAYDGAWDCAVKTVKAEGAMALYKGFVPTVCRQGPFTVVLV 301

Query: 299 FLEQMKNK 305
LEQ+ K
Sbjct: 302 TLEQVRK 308

Score = 48.1 bits (113), Expect = 3e-04
Identities = 43/184 (23%), Positives = 74/184 (40%), Gaps = 11/184 (5%)

Query: 31 AGMGATVFVQPLDLVKNRMLSGEG--AKTREYKTSFHALTSILKAEGLRGIYTGLSAGL 88
G+GA V P D+ RMQ G A+ R Y A+ S++K EG+ ++ G + +
Sbjct: 137 GGIGAAVG-NPADVAMVRMQADGRLPLAQRRNYAGVGDAIRSMVKGEVTSLWRGSALTI 195

Query: 89 LRQATYTTTTLRGLIYTVLFRERLTGADGTTPPGFLLKAVIGMTAGATGAFVGTAEVALIRMT 148
R T +L Y E + G V AG + P +V R+
Sbjct: 196 NRAMIVTAAQLASYDQFKEGILENGVMNDGLGTHVVASFAAGFVASVASNPVDVIKTRVM 255

Query: 149 ADGRLPADQRRG-YKNVFNALIRITREEGVLTWRGCIPTMARAVVVNAAQLASYSQSKQ 207
+ + G Y ++ ++ + EG + L++G +PT+ R + Q ++
Sbjct: 256 -----NMKVGAYDGAWDCAVKTVKAEGAMALYKGFVPTVCRQGPFTVVLFTLEQVRK 308

Query: 208 FLLD 211
L D
Sbjct: 309 LLRD 312

>gi|50545838|ref|XP_500457.1| hypothetical protein [Yarrowia lipolytica]
gi|49646323|emb|CAG82683.1| unnamed protein product [Yarrowia lipolytica]
Length = 320

Score = 204 bits (518), Expect = 3e-51
Identities = 119/301 (39%), Positives = 172/301 (57%), Gaps = 18/301 (5%)

Query: 16 PRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAE 75
P ++ F +GG A + A VF PLDL K R+Q AKTR + F L +++K E
Sbjct: 25 PPSAKIHYPFWYGGFASVVAGVFTHPLDLAKVRLQT----AKTRG-QGLFGTLVNVVKHE 79

Query: 76 GLRGIYTGLSAGLLRQATYTTTTLRGIYTVLFRERLT-----GADGTPPGFLLKAVIGMT 128
G+ G+Y+GLSA +LR +TY+T R G+Y L E + D PP ++L I +
Sbjct: 80 GITGVYSGLSASMLRLSTYSTMRFGMYEYLKESIAPYYNPNKRDQNPPMYVLLP-ISII 138

Query: 129 AGATGAFVGTTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLGCIPTM 188
AG +G VG PA++ IRM D LP DQRR YK+ F+ LIR+ +EEGV ++RG P
Sbjct: 139 AGISGGIVGNPADIINIRMQNDQSLPKDQRRNYKHAFDGLIRMYKEEGVRAMFRGLGPNC 198

Query: 189 ARAVVVNAAQLASYSQSKQFLLDS-GYFSDNILCHFCASMISGLVTTAASMPVDIAKTRI 247
R V++ ++Q+ SY K L++ G D HF AS+++GL+ T PVD+ KTRI
Sbjct: 199 TRGVLMTSSQMVSYSDFKALLVNHLGMNPDKKATHFSASLLAGLMATTVCSPVDVVKTRI 258

Query: 248 QNMRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFLEQMKNKAY 307
N K + + F ++ EG +++G+ P + RLGP T+LT+I LEQ+ K Y
Sbjct: 259 MNAHAHHSK---DSAFTIFFNALKQEGPLFMFRGWLPFVRLGPQTILTYIVLEQL-KFY 314

Query: 308 K 308
K
Sbjct: 315 K 315

>gi|49088466|ref|XP_406054.1| hypothetical protein AN1917.2 [Aspergillus nidulans]
gi|40745926|gb|EAA65082.1| hypothetical protein AN1917.2 [Aspergillus nidulans FG
Length = 314

Score = 201 bits (512), Expect = 1e-50
Identities = 117/288 (40%), Positives = 169/288 (58%), Gaps = 6/288 (2%)

Query: 22 SVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIY 81
++ F+ GGLAGM ATV +QP+D++K R+QL+GEG +T ++ +I+ + + +Y
Sbjct: 24 ALPFINGGLAGMTATVVIQPIDMIKVRQLAGEGVRTGPRPSALGVARNIIASGKVLDLY 83

Query: 82 TGLSAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPP---GFLLKAVIGMTAGATGAFVGT 138
TGLSAGLLRQA YTT RLG + + LT T F +A G+TAG A +G
Sbjct: 84 TGLSAGLLRQAVYTTARLGFFDTFMKALTKNADTANRKVTFAERAGAGLTAGGIAAMIGN 143

Query: 139 PAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLGCIPTMARAVVVNAAQ 198
PA++AL+RM +DG P + R Y++V +AL RI++ EGV LW G PT+ RA+ +N Q
Sbjct: 144 PADLALVRMQSDGLKPPEARAHYRSVIDALFRISKAEGVTALWAGAFPTVVRAMALNLGQ 203

Query: 199 LASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRM--IDGK 256

LA +++SK L S F AS I+G + S+P D KTR+Q + G+
 Sbjct: 204 LAFFAESKAQLKTRTSLSAQNQT-FAASAIAGFFASFLSLPFDVVKTRLQKQKDPKTGQ 262

Query: 257 PEYKNGLDVLFKVVR YEGFFSLWKGFTPYYARLGPHTVLT FIFLEQMN 304
 YK D KVV R EG+ ++GF YY R+ PH ++T I + +N
 Sbjct: 263 LPYKGMFDCARKVVRDEGWLFYRGFGTYVRIAPHAMVTLIVADYLN 310

Score = 33.1 bits (74), Expect = 8.9
 Identities = 26/89 (29%), Positives = 38/89 (42%), Gaps = 4/89 (4%)

Query: 15 KPRTS--PKSVKFLFGGLAGMGATV FVQPLDLVK NRMQLSGEGAKTRE--YKTSFHALTS 70
 K RTS ++ F +AG A+ P D VK R+Q + KT + YK F
 Sbjct: 215 KTRTSLSAQNQTFAASAIAGFFASFLSLPFDVVKTRLQKQKDPKTGQLPYKGMFDCARK 274

Query: 71 ILKAEGLRGIYTGLSAGLLRQATYTTTTRL 99
 +++ EG Y G +R A + L
 Sbjct: 275 VVRDEGWLFYRGFGTYVRIAPHAMVTL 303

>gi|46806315|dbj|BAD17507.1| 2-oxoglutarate carrier-like protein [Oryza sativa (ja
 cultivar-group)]
 Length = 321

Score = 201 bits (511), Expect = 2e-50
 Identities = 130/312 (41%), Positives = 179/312 (57%), Gaps = 28/312 (8%)

Query: 25 FLFGGLAGMGATV FVQPLDLVK NRMQLSGEGAKTREYK----- 62
 F+ GG A + A PLDL+K RMQL GEG
 Sbjct: 6 FVEGGAACVVGASCTHPLDLIKVRMQLHGEGPPAPALAFPGGGAHHHHHHLLQQQPPRR 65

Query: 63 -TSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTRLGIYTVL---FERLTGADGTTPPG 118
 IL+AEG G+ +G+SA +LRQ Y+TT +G+Y L +ER G G P
 Sbjct: 66 PGPIAVCAQILRAEGPTGLLSGV SATMLRQTLYSTTCMGLYDTLKRRWERDDGGGGGGLP 125

Query: 119 FLLKAVIGMTAGATGAFVGTAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGV 178
 K G+ +G GA VG PA+VA++RM ADGRLPA QRR Y++V +A++R+ R+EGV
 Sbjct: 126 LHRKVAAGLFSGGVGAAVGNPADVAMVRMQADGRLPAAQRRNYRSVADAIVRMARDEGVC 185

Query: 179 TLWRGCIPTMARAVVVNAAQLASYSQSKQFLL-DSGYFSDNILCHFCASMISGLVTTAAS 237
 +LWRG T+ RA++V A+QLA+Y Q+K+ +L G +D + H A + +GLV +AS
 Sbjct: 186 SLWRGSPLTVKRAMIVAASQLATYDQAKEAILARRGQGADGLATHVAAGLAAGLVAASAS 245

Query: 238 MPVDIAKTRIQNMRMIDGK-PEYKNGLDVLFKVVR YEGFFSLWKGFTPYYARLGPHTVLT 296
 PVD+ KTR+ NM+++ G P Y LD L K VR EG +L+KGF P R GP T++
 Sbjct: 246 TPVDVVKTRVMNMKV VAGAPPPYSGALDCLIKTVRSEGAMALYKGFVPTVTRQGPFTIVL 305

Query: 297 FIFLEQMKNKAYK 308
 F+ LEQ+ K K
 Sbjct: 306 FVTLEQVRKLLK 317

>gi|32407105|ref|XP_324149.1| hypothetical protein [Neurospora crassa]
 gi|28921909|gb|EAA31182.1| hypothetical protein [Neurospora crassa]
 Length = 1796

Score = 201 bits (510), Expect = 2e-50

Identities = 116/294 (39%), Positives = 166/294 (56%), Gaps = 5/294 (1%)

Query: 22 SVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIY 81
 ++ F+ GGL+GM AT +QP+D++K R+QL+GEG T I+ + +Y
 Sbjct: 42 ALPFINGGLSGMVATTVIQPIDMIKVRIQLAGEGKAGGPKPTPLGVTRDIIASGKAMDLY 101

Query: 82 TGLSAGLLRQATYTTTTLRGIYTVLFRERLTG---ADGTPPGFLLKAVIGMTAGATGAFVGT 138
 TGLSAGLLRQA YTT R+G + RL+ G GF +A G+ AG A +G
 Sbjct: 102 TGLSAGLLRQAVYTTARIGCFDTFMSRLSARAKEKGQSVGFKERASAGLAAGGLAAMIGN 161

Query: 139 PAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWRCIPTMARAVVVNAAQ 198
 PA++ALIRM +DG P +R+ YK+V +AL I R EGV LW G PT+ RA+ +N Q
 Sbjct: 162 PADLALIRMQSDGLKPVAERKNYKSVIDALGGIARNEGVAALWAGAAPTVVRAMALNFGQ 221

Query: 199 LASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNM-RMIDGKP 257
 LA +S++K L +S + AS I+G + S+P D KTR+Q R DGK
 Sbjct: 222 LAFFSEAKAQLKARTQWSSKVQT-LSASAIAGFFASFFSLPFDVFKTRLQKQTRGPDGKL 280

Query: 258 EYKGLDVLFKVVRVYEGFFSLWKGFTPYYARLGPHTVLTFFIFLEQMKNKAYKRLF 311
 Y +D KV + EG F ++GF YY R+ PH ++T + + + K++F
 Sbjct: 281 PYNGMVDCFAKVAKQEGVFRFYRGFGTYVRIAPHAMVTLLVADYLGWLTKQMF 334

>gi|24637836|gb|AAN63885.1| **L** brain mitochondrial carrier protein short-inserted f
 musculus]
 Length = 353

Score = 197 bits (500), Expect = 3e-49
 Identities = 115/309 (37%), Positives = 169/309 (54%), Gaps = 20/309 (6%)

Query: 2 AATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTR-- 59
 ++T S G++ KP F++GGLA + A P+DL K R+Q+ G+ R
 Sbjct: 57 SSTLSHEMSGLNWKP-----FVYGGLASIVAEFGTFPVDLTKTRLQVQGSIDVRFK 108

Query: 60 --EYKTSFHALTSILKAEGLRGIYTGSLSAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPP 117
 +Y+ FHAL I K EG+ +Y+G++ LLRQA+Y T ++GIY L +RL
 Sbjct: 109 EIKYRGMFHALFRIYKEEGILALYSGIAPALLRQASYGTIKIGIYQSL-KRLFVERLEDE 167

Query: 118 GFLKAVIGMTAGATGAFVGTPEAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGV 177
 L+ + G+ +G + + P +V IRM A G L G + I I ++EG
 Sbjct: 168 TLLINMICGVVSGVISSTIANPTDVLKIRMQAQGSLSFQGS MIG-----SFIDIYQQEGT 221

Query: 178 LTLWRCIPTMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAAS 237
 LWRG +PT RA +V +L Y +K+ L+ SG D IL HF +S GL AS
 Sbjct: 222 RGLWRGVVPTAQRAAIVVGVELPVYDITKKHLIVSGMLGDTILTHFVSSFTCGLAGALAS 281

Query: 238 MPVDIAKTRIQNMRMIDGKPE-YKGLDVLFKVVRVYEGFFSLWKGFTPYYARLGPHTVLT 296
 PVD+ +TR+ N R I G + YK LD + K+ ++EGFF+L+KGF P + RLGP ++
 Sbjct: 282 NPVDVVRTRMMNQRAIVGHVDLYKGTLDGILKMWKHEGFFALYKGFWPWNWRLGPWNIIIF 341

Query: 297 FIFLEQMKN 305
 FI EQ+ +
 Sbjct: 342 FITYEQLKR 350

Score = 37.0 bits (84), Expect = 0.54
 Identities = 24/94 (25%), Positives = 44/94 (46%), Gaps = 8/94 (8%)

Query: 223 FCASMISGLVTTAASMPVDIAKTRIQ-NMRMID---GKPEYKNGLDVLFKVVRYEGFFSL 278
 F ++ +V + PVD+ KTR+Q + ID + +Y+ LF++ + EG +L
 Sbjct: 72 FVYGGASIVAEFGTFPVDLTKTRLQVQGSIDVRFKEIKYRGMFHALFRIYKEEGILAL 131

Query: 279 WKGFTPYARLGPHTVLTFFIFLEQMKNKAYKRLFL 312
 + G P R + + + + KRLF+
 Sbjct: 132 YSGIAPALLRQASYGTIKIGIYQSL----KRLFV 161

>gi|24637838|gb|AAN63886.1| **L** brain mitochondrial carrier protein long-inserted fo
 musculus]
 Length = 356

Score = 196 bits (499), Expect = 4e-49
 Identities = 115/309 (37%), Positives = 169/309 (54%), Gaps = 20/309 (6%)

Query: 2 AATASAGAGGIDGKPRTPSKSVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTR-- 59
 ++T S G++ KP F++GGLA + A P+DL K R+Q+ G+ R
 Sbjct: 60 SSTLSHEMSGLNWKP-----FVYGGASIVAEFGTFPVDLTKTRLQVQGSIDVRFK 111

Query: 60 --EYKTSFHALTSILKAEGLRGIYTGSLAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPP 117
 +Y+ FHAL I K EG+ +Y+G++ LLRQA+Y T ++GIY L +RL
 Sbjct: 112 EIKYRGMFHALFRIYKEEGILALYSGIAPALLRQASYGTIKIGIYQSL-KRLFVERLEDE 170

Query: 118 GFLKAVIGMTAGATGAFVGTPEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGV 177
 L+ + G+ +G + + P +V IRM A G L G + I I ++EG
 Sbjct: 171 TLLINMICGVVSGVISSTIANPTDVLKIRMQAQGSILFQGSIMIG-----SFIDIYQQEGT 224

Query: 178 LTLWRGCIPTMARAVVVNAAQLASYSQSKQFLDSDGYFSDNILCHFCASMISGLVTTAAS 237
 LWRG +PT RA +V +L Y +K+ L+ SG D IL HF +S GL AS
 Sbjct: 225 RGLWRGVVPTAQRAAIVVGVELPVYDITKKHLIVSGMLGDTILTHFVSSFTCTGLAGALAS 284

Query: 238 MPVDIAKTRIQNMRMIDGKPE-YKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLT 296
 PVD+ +TR+ N R I G + YK LD + K+ ++EGFF+L+KGF P + RLGP ++
 Sbjct: 285 NPVDVVRTRMMNQRAIVGHVDLYKGTLDGILKMWKHEGFFALYKGFWPWNWRLGPWNIIF 344

Query: 297 FIFLEQMKNK 305
 FI EQ+ +
 Sbjct: 345 FITYEQLKR 353

Score = 37.0 bits (84), Expect = 0.57
 Identities = 24/94 (25%), Positives = 44/94 (46%), Gaps = 8/94 (8%)

Query: 223 FCASMISGLVTTAASMPVDIAKTRIQ-NMRMID---GKPEYKNGLDVLFKVVRYEGFFSL 278
 F ++ +V + PVD+ KTR+Q + ID + +Y+ LF++ + EG +L
 Sbjct: 75 FVYGGASIVAEFGTFPVDLTKTRLQVQGSIDVRFKEIKYRGMFHALFRIYKEEGILAL 134

Query: 279 WKGFTPYARLGPHTVLTFFIFLEQMKNKAYKRLFL 312
 + G P R + + + + KRLF+
 Sbjct: 135 YSGIAPALLRQASYGTIKIGIYQSL----KRLFV 164

>gi|46127995|ref|XP_388551.1| hypothetical protein FG08375.1 [Gibberella zeae PH-1]
 gi|42549320|gb|EAA72163.1| hypothetical protein FG08375.1 [Gibberella zeae PH-1]
 Length = 325

Score = 196 bits (497), Expect = 9e-49

Identities = 115/281 (40%), Positives = 165/281 (58%), Gaps = 5/281 (1%)

Query: 22 SVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIY 81
 ++ F+ GG+AGM AT +QP+D+VK R+QL+GEG T + I+ + +Y
 Sbjct: 36 ALPFINGGIAGMVATTVIQPVDMVKVRIQLAGEGTATGPKPSPLAVTRQIIASGKFLDLY 95

Query: 82 TGLSAGLLRQATYTTTTRLGIYTVLFLERLTG---ADGTPPGFLLKAVIGMTAGATGAFVGT 138
 TGLSAGLLRQA YTT RLG++ L L+ +G GF +A G+TAG A +G
 Sbjct: 96 TGLSAGLLRQAVYTTARLGMFDTLMGNLSARAKTEGRTVGFKERATAGLTAGGIAAMIGN 155

Query: 139 PAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRGCIPTMARAVVVNAAQ 198
 PA++ALIRM +DG P +R+ YK+V +AL I + EGV LW G PT+ARA+ +N Q
 Sbjct: 156 PADLALIRMQSDGLKPLAERKNYKSVIDALSSIASEGVGALWAGAAPTVARAMALNFGQ 215

Query: 199 LASYSQSKQFLLD SGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNM-RMIDGKP 257
 LA +S++K L + S AS ++G + S+P D KTR+Q + DGK
 Sbjct: 216 LAFFSEAKVQLKKNLTDLSARTQT-LTASAVAGFFASFFSLPFDVFKTRLQKQSKGPDGKL 274

Query: 258 EYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFI 298
 Y++ +D KV + EG ++GF YY R+ PH ++T I
 Sbjct: 275 PYRSMIDCFSKVAKQEGLRGFRYRGFTYYVRIAPHAMVTLI 315

>gi|50423171|ref|XP_460166.1| unnamed protein product [Debaryomyces hansenii]
 gi|49655834|emb|CAG88439.1| unnamed protein product [Debaryomyces hansenii]
 Length = 290

Score = 195 bits (496), Expect = 1e-48

Identities = 109/282 (38%), Positives = 161/282 (57%), Gaps = 10/282 (3%)

Query: 25 FLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIYTGL 84
 F +GG A M A + PLDL K R+Q + + ++ + I+ EG IY+GL
 Sbjct: 12 FWYGAASMVACLVTPLDLAKVRLQTASKPGQSLG----SMVYQIITKEGFLKIYSGL 66

Query: 85 SAGLLRQATYTTTTRLGIYTVLFLERLTGADGTPPGFLLKAVIGMTAGATGAFVGTAEVAL 144
 SA LLRQATY+T R GIY L E T T P + + M AGA G +G P++V
 Sbjct: 67 SASLLRQATYSTARFGIYEFLKETYTEKYHTTSTGILLPMSMVAGALGGLIGNPSDVVN 126

Query: 145 IRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRGCIPTMARAVVVNAAQLASYSQ 204
 IRM D LP +QRR Y+N F+ + RI +EE V +L+RG +P + R V++ A+Q+ +Y
 Sbjct: 127 IRMQNDSSLPIEQRRNYRNAFDGIFRIIKEEKVSSLFRGLVPNLTRGVLMTASQVVYDI 186

Query: 205 SKQFLLD SGYFS-DNILCHFCASMISGLVTTAASMPVDIAKTRIQNM RMIDGKPEYKNGL 263
 +K L+D+ + HF AS+++GLV T P D+ KTRI N + + +
 Sbjct: 187 AKNLLVDLHLDP SKKATHFSASLLAGLVATTVCSPADVVKTRIMNAK---GASNGSTI 242

Query: 264 DVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLT FIFLEQM NK 305
 +L V+ EG +++G+ P + RLGPH T++TF+ LEQ+ K
 Sbjct: 243 SILTSAVKTEGVGFMRGWLPSFIRLGPHTIVTFLALEQLRK 284

Score = 33.9 bits (76), Expect = 5.0

Identities = 24/77 (31%), Positives = 36/77 (46%), Gaps = 4/77 (5%)

Query: 19 SPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLR 78
 S K+ F LAG+ AT P D+VK R+ AK ++ LTS +K EG+
 Sbjct: 200 SKKATHFSASLLAGLVATTVCSPADVVKTRIM---NAKGASNGSTISILTSAVKTEGVG 255

Query: 79 GIYTGLSAGLLRQATYT 95
 ++ G +R +T
 Sbjct: 256 FMFRGWLPSPFIRLGPHT 272

>gi|20149598|ref|NP_036272.2| **[L]** solute carrier family 25 (mitochondrial carrier; d
 transporter), member 10; dicarboxylate ion carrier [Homo
 sapiens]
 gi|20137671|sp|Q9UBX3|DIC HUMAN **[L]** Mitochondrial dicarboxylate carrier
 gi|13938431|gb|AAH07355.1| **[L]** Solute carrier family 25 (mitochondrial carrier; dic
 transporter), member 10 [Homo sapiens]
 gi|22761214|dbj|BAC11497.1| **[L]** unnamed protein product [Homo sapiens]
 Length = 287

Score = 194 bits (493), Expect = 2e-48
 Identities = 110/284 (38%), Positives = 156/284 (54%), Gaps = 11/284 (3%)

Query: 24 KFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIYTG 83
 ++ FGGLA GA PLDL+K +Q E K R + +++ +G+ +Y+G
 Sbjct: 9 RWFYFGGLASCGAACCTHPLDLLKVHLQTQQE-VKLRMTGMALR----VVRTDGILALYSG 63
 Query: 84 LSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGATGAFVGTPAEVA 143
 LSA L RQ TY+ TR IY + +R+ P F K ++G +G G FVGTPA++
 Sbjct: 64 LSASLCRQMTYSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVGTGPADLV 123
 Query: 144 LIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRCIPTMARAVVVNAAQLASYS 203
 +RM D +LP QRR Y + + L R+ REEG+ L+ G +R +V QL+ Y
 Sbjct: 124 NVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLFSGATMASSRGALVTVGQLSCYD 183
 Query: 204 QSKQFLLDSDGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGKPEYKNGL 263
 Q+KQ +L +GY SDNI HF AS I+G T P+D+ KTR+ N K EY+
 Sbjct: 184 QAKQLVLSTGYLSDNIFTHFVASFIAGGCATFLCQPLDVLKTRLMN-----SKGEYQGVF 238
 Query: 264 DVLFKVVRYEGFFSLWKGFPPYARLGPHTVLTFFIFLEQMKNKAY 307
 + + G + +KG P RL PHTVLTFF+FLEQ+ K +
 Sbjct: 239 HCAVETAKL-GPLAFYKGLVPAGIRLIPHTVLTFFVFLEQLRKNF 281

Score = 48.5 bits (114), Expect = 2e-04
 Identities = 41/175 (23%), Positives = 69/175 (39%), Gaps = 10/175 (5%)

Query: 20 PKSVKFLFGGLAGMGATVFVQPLDLVKNRMQ--LSGEGAKTREYKTSFHALTSILKAEGL 77
 P K L G ++G+ P DLV RMQ + + R Y + L + + EGL
 Sbjct: 98 PFHEKVLLGSVSGLAGGFVGTGPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGL 157
 Query: 78 RGIYTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGATGAFVG 137
 R +++G + R A T +L Y + + V AG F+
 Sbjct: 158 RRLFSGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVASFIAGGCATFLC 217
 Query: 138 TPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRCIPTMARAV 192
 P +V R+ + + Y+ VF+ + T + G L ++G +P R +
 Sbjct: 218 QPLDVLKTRLM-----NSKGEYQGVFHCAGE-TAKLGPLAFYKGLVPAGIRLI 264

>gi|50745529|ref|XP_420143.1| PREDICTED: similar to solute carrier family 25, memb

UCP5S; brain mitochondrial carrier protein 1;
mitochondrial uncoupling protein 5 [Gallus gallus]
Length = 711

Score = 193 bits (490), Expect = 5e-48
Identities = 111/286 (38%), Positives = 157/286 (54%), Gaps = 12/286 (4%)

Query: 25 FLFGGLAGMGATVFVQPLDLVKNMQLSGEGAKTR----EYKTSFHALTSILKAEGLRGI 80
F++GGLA + A P+DL K R+Q+ G+ A R Y+ FHAL I + EG R +
Sbjct: 430 FVYGGLASIVAEFGTFPVDLTKTRLQVQGSADARFREVRYRGMFHALFRICREEGGRAL 489

Query: 81 YTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGATGAFVGTTPA 140
Y+G++ LLRQA+Y T ++GIY L +RL L+ + G+ +G + + P
Sbjct: 490 YSGIAPALLRQASYGTIKIGIYQSL-KRLFVDRLEDETLLINVICGVVSGVISSALANPT 548

Query: 141 EVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWRCIPTMARAVVVNAAQLA 200
+V IRM A G L + + I I ++EG LWRG +PT RA +V +L
Sbjct: 549 DVLKIRMQAQGNLFQG-----GMIGSFIDIYQQEGTRGLWRGVVPTAQRAAIVVGVELP 602

Query: 201 SYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGKPE-Y 259
Y +K+ L+ SG D I HF +S GL AS PVD+ +TR+ N R I G E Y
Sbjct: 603 VYDITKKHLILSGLMGDTIFTHFVSSFTCGLAGAIASNPVDVVRTRMMNQRAIVGSEVELY 662

Query: 260 KNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFFIFLEQMNK 305
K LD L K + EGFF+L+KGF P + RLGP ++ FI EQ+ +
Sbjct: 663 KGTLDGLVKTWKSEGFFALYKGFWPWNWLRGLGPWNIIFFITYEQLKR 708

Score = 52.8 bits (125), Expect = 1e-05
Identities = 44/189 (23%), Positives = 73/189 (38%), Gaps = 11/189 (5%)

Query: 23 VKFLFGGLAGMGATVFVQPLDLVKNMQLSG---EGAKTREYKTSFHALTSILKAEGLRG 79
+ + G ++G+ ++ P D++K RMQ G +G + I + EG RG
Sbjct: 529 INVICGVVSGVISSALANPTDVLKIRMQAQGNLFQGGMIGSF-----IDIYQQEGTRG 581

Query: 80 IYTGLSAGLLRQATYTTTTRLGIYTVLFERLTGADGTPPGFLLKAVIGMTAGATGAFVGTTP 139
++ G+ R A L +Y + + L + V T G GA P
Sbjct: 582 LWRGVVPTAQRAAIVVGVELPVYDITKKHLILSGLMGDTIFTHFVSSFTCGLAGAIASNP 641

Query: 140 AEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWRCIPTMARAVVVNAAQL 199
+V RM + R YK + L++ + EG L++G P R N
Sbjct: 642 VDVVRTRMM-NQRAIVGSEVELYKGTLDGLVKTWKSEGFFALYKGFWPWNWLRGLGPWNIIFF 700

Query: 200 ASYSQSKQF 208
+Y Q K+
Sbjct: 701 ITYEQLKRL 709

>gi|6179584|emb|CAB59892.1| **L** dicarboxylate carrier protein [Homo sapiens]
gi|6224534|emb|CAB60007.1| **L** dicarboxylate carrier protein [Homo sapiens]
Length = 287

Score = 193 bits (490), Expect = 5e-48
Identities = 110/284 (38%), Positives = 156/284 (54%), Gaps = 11/284 (3%)

Query: 24 KFLFGGLAGMGATVFVQPLDLVKNMQLSGEGAKTREYKTSFHALTSILKAEGLRGIYTG 83
++ FGGLA GA PLDL+K +Q E K R + +++ +G+ +Y+G

Sbjct: 9 RWFYGGGLASCGAACCTHPLDLLKVHLQTQQE-VKLRMTGMALR----VVRTDGILALYSG 63

Query: 84 LSAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFVGTPEVA 143
LSA L RQ TY+ TR IY + +R+ P F K ++G +G G FVGTPA++

Sbjct: 64 LSASLCRQMTYSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGVSGLAGGFVGTADLV 123

Query: 144 LIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLRGCIPTMARAVVVNAAQLASYS 203
+RM D +LP QRR Y + + L R+ REEG+ L+ G +R +V QL+ Y

Sbjct: 124 NVRMQNDVKLPQGGRRNYAHALDGLYRVAREEGLRRLFSGATMASSRGALVTVGQLSCYD 183

Query: 204 QSKQFLLDGSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGKPEYKNGL 263
Q+KQ +L +GY SDNI HF AS I+G T P+D+ KTR+ N K EY+

Sbjct: 184 QAKQRLSTGYLSDNIFTHFVASFIAGGCATFLCQPLDVLKTRLMN-----SKGEYQGVF 238

Query: 264 DVLFKVRYEGFFSLWKGFPTPYARLGPHTVLTFFLEQMKNKAY 307
+ + G + +KG P RL PHTVLTFFLEQ+ K +

Sbjct: 239 HCAVETAKL-GPLAFYKGLVPAGIRLIPHTVLTFFLEQLRKNF 281

Score = 51.2 bits (121), Expect = 3e-05
Identities = 42/175 (24%), Positives = 70/175 (40%), Gaps = 10/175 (5%)

Query: 20 PKSVKFLFGGLAGMGATVVFQPLDLVKNRMQ--LSGEGAKTREYKTSFHALTSILKAEGL 77
P K L G ++G+ P DLV RMQ + + R Y + L + + EGL

Sbjct: 98 PFHEKVLLGVSGLAGGFVGTADLVNVRMQNDVKLPQGGRRNYAHALDGLYRVAREEGL 157

Query: 78 RGIYTGLSAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFVG 137
R +++G + R A T +L Y +R+ V AG F+

Sbjct: 158 RRLFSGATMASSRGALVTVGQLSCYDQAKQRLSTGYLSDNIFTHFVASFIAGGCATFLC 217

Query: 138 TPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTWLRGCIPTMARAV 192
P +V R+ + + Y+ VF+ + T + G L ++G +P R +

Sbjct: 218 QPLDVLKTRLM-----NSKGEYQGVFHCVE-TAKLGPLAFYKGLVPAGIRLI 264

>gi|6755544|ref|NP_035528.1| **L** solute carrier family 25 (mitochondrial carrier, br
solute carrier family 25 (mitochondrial carrier, brain)
member 14 [Mus musculus]

gi|4139057|gb|AAD03674.1| **L** brain mitochondrial carrier protein BMCP1 [Mus muscul

gi|11094343|gb|AAG29586.1| **L** mitochondrial uncoupling protein 5 short form [Mus m
Length = 322

Score = 193 bits (490), Expect = 5e-48
Identities = 115/309 (37%), Positives = 169/309 (54%), Gaps = 20/309 (6%)

Query: 2 AATASAGAGGIDGKPRTPSPKSVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTR-- 59
++T S G++ KP F++GGLA + A P+DL K R+Q+ G+ R

Sbjct: 26 SSTLSHEMSGLNWKP-----FVYGGLASIVAEFGTFPVDLTKTRLQVQGSIDVRFK 77

Query: 60 --EYKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTTLRGIYTVLFRERLTGADGTPP 117
+Y+ FHAL I K EG+ +Y+G++ LLRQA+Y T ++GIY L +RL

Sbjct: 78 EIKYRGMFHALFRIYKEEGILALYSGIAPALLRQASYGTIKIGIYQSL-KRLFVERLEDE 136

Query: 118 GFLKAVIGMTAGATGAFVGTPEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGV 177
L+ + G+ +G + + P +V IRM A G L G + I I ++EG

Sbjct: 137 TLLINMICGVVSGVISSTIANPTDVLKIRMQAQGSLSFGSMIG-----SFIDIYQQEGT 190

Query: 178 LTLWRGCIPTMARAVVNAACLASYQSQKQFLDLSGYFSDNILCHFCASMISGLVTTAAS 237
 LWRG +PT RA +V +L Y +K+ L+ SG D IL HF +S GL AS
 Sbjct: 191 RGLWRGVVPTAQRAAIVVGVELPVYDITKKHLIVSGMLGDTILTHFVSSFTCGLAGALAS 250

Query: 238 MPVDIAKTRIQNMIDGKPE-YKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLT 296
 PVD+ +TR+ N R I G + YK LD + K+ ++EGFF+L+KGF P + RLGP ++
 Sbjct: 251 NPVDVVRTRMMNQRAIVGHVDLYKGTLDGILKMWKHEGFFALYKGFWPWNWRLRGPWNIIIF 310

Query: 297 FIFLEQMNK 305
 FI EQ+ +
 Sbjct: 311 FITYEQLKR 319

Score = 36.2 bits (82), Expect = 1.0
 Identities = 24/94 (25%), Positives = 44/94 (46%), Gaps = 8/94 (8%)

Query: 223 FCASMISGLVTTAASMPVDIAKTRIQ-NMRMID---GKPEYKNGLDVLFKVVRYEGFFSL 278
 F ++ +V + PVD+ KTR+Q + ID + +Y+ LF++ + EG +L
 Sbjct: 41 FVYGLASIVAEFGTFPVDLTKTRLQVQGSIDVRFKEIKYRGMFHALFRIYKEEGILAL 100

Query: 279 WKGFTPYARLGPHTVLTFFIFLEQMNKAYKRLFL 312
 + G P R + + + + KRLF+
 Sbjct: 101 YSGIAPALLRQASYGTIKIGIYQSL----KRLFV 130

>gi|20141977|sp|Q9Z2B2|UCP5 MOUSE **L** Brain mitochondrial carrier protein-1 (BMCP-1)
 uncoupling protein 5) (UCP 5) (Solute carrier family 25,
 member 14)

gi|11094341|gb|AAG29585.1| **L** mitochondrial uncoupling protein 5 long form [Mus mu
 gi|28913739|gb|AAH48692.1| **L** Slc25a14 protein [Mus musculus]
 Length = 325

Score = 193 bits (490), Expect = 5e-48
 Identities = 115/309 (37%), Positives = 169/309 (54%), Gaps = 20/309 (6%)

Query: 2 AATASAGAGGIDGKPRTSVKFGLFGLAGMGATVFVQPLDLVKNRMQLSGEGAKTR-- 59
 ++T S G++ KP F++GGLA + A P+DL K R+Q+ G+ R
 Sbjct: 29 SSTLSHEMSGLNWKP-----FVYGLASIVAEFGTFPVDLTKTRLQVQGSIDVRFK 80

Query: 60 --EYKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFRERLTGADGTPP 117
 +Y+ FHAL I K EG+ +Y+G++ LLRQA+Y T ++GIY L +RL
 Sbjct: 81 EIKYRGMFHALFRIYKEEGILALYSGIAPALLRQASYGTIKIGIYQSL-KRLFVERLEDE 139

Query: 118 GFLLKAVIGMTAGATGAFVGTPEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGV 177
 L+ + G+ +G + + P +V IRM A G L G + I I ++EG
 Sbjct: 140 TLLINMICGVVSGVISSTIANPTDVLKIRMQAQGSLSFQGS MIG-----SFIDIYQQEGT 193

Query: 178 LTLWRGCIPTMARAVVNAACLASYQSQKQFLDLSGYFSDNILCHFCASMISGLVTTAAS 237
 LWRG +PT RA +V +L Y +K+ L+ SG D IL HF +S GL AS
 Sbjct: 194 RGLWRGVVPTAQRAAIVVGVELPVYDITKKHLIVSGMLGDTILTHFVSSFTCGLAGALAS 253

Query: 238 MPVDIAKTRIQNMIDGKPE-YKNGLDVLFKVVRYEGFFSLWKGFTPYARLGPHTVLT 296
 PVD+ +TR+ N R I G + YK LD + K+ ++EGFF+L+KGF P + RLGP ++
 Sbjct: 254 NPVDVVRTRMMNQRAIVGHVDLYKGTLDGILKMWKHEGFFALYKGFWPWNWRLRGPWNIIIF 313

Query: 297 FIFLEQMNK 305
 FI EQ+ +

Sbjct: 314 FITYEQLKR 322

Score = 36.2 bits (82), Expect = 1.0
Identities = 24/94 (25%), Positives = 44/94 (46%), Gaps = 8/94 (8%)

Query: 223 FCASMISGLVTTAASMPVDIAKTRIQ-NMRMID---GKPEYKNGLDVLFKVVRYEGFFSL 278
F ++ +V + PVD+ KTR+Q + ID + +Y+ LF++ + EG +L
Sbjct: 44 FVYGGLASIVAEFGTFPVDLTKTRLQVQGSIDVRFKEIKYRGMFHALFRIYKEEGILAL 103

Query: 279 WKGFPTPYARLGPHTVLTFFIFLEQMKNKAYKRLFL 312
+ G P R + + + + KRLF+
Sbjct: 104 YSGIAPALLRQASYGTIKIGIYQSL----KRLFV 133

>gi|19173788|ref|NP_596909.1| **[L]** solute carrier family 25 (mitochondrial carrier; d
transporter), member 10 [Rattus norvegicus]
gi|3646426|emb|CAA11278.1| **[L]** mitochondrial dicarboxylate carrier [Rattus norvegicus]
Length = 286

Score = 192 bits (489), Expect = 6e-48
Identities = 110/287 (38%), Positives = 157/287 (54%), Gaps = 11/287 (3%)

Query: 21 KSVKFLFGGLAGMGATVVFQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGI 80
++ ++ FGGLA GA PLDL+K +Q E K R + +++ +G +
Sbjct: 5 RTSRWYFGGLASCGAACCTHPLDLLKVHLQTQQE-VKLRMTGMALQ----VVRTDGFLAL 59

Query: 81 YTGLSAGLLRQATYTTTRLGIYTVLFRERLTGADGTPPGFLLKAVIGMTAGATGAFVGTPA 140
Y GLSA L RQ TY+ TR IY + + +T P F K ++G +G TG FVGTPA
Sbjct: 60 YNGLSASLCRQMTYSLTRFAIYETMRDYMTKDSQGPLPFYSKVLLGGISGLTGGFVGTPA 119

Query: 141 EVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVTLWRGCIPTMARAVVVNAAQLA 200
++ +RM D +LP QRR Y + + L R+ REEG+ L+ G +R +V QL+
Sbjct: 120 DLNVNRMQNDMKLPLSQRRNYSHALDGLYRVAREEGLKKLFSGATMASSRGALVTVGQLS 179

Query: 201 SYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGKPEYK 260
Y Q+KQ +L +GY SDNI HF +S I+G T P+D+ KTR+ N K EY+
Sbjct: 180 CYDQAKQLVLSTGYLSDNIFTHFLSSFIAGGCATFLCQPLDVLKTRLMN-----SKGEYQ 234

Query: 261 NGLDVLFKVVRYEGFFSLWKGFPTPYARLGPHTVLTFFIFLEQMKNKAY 307
+ + G + +KG P RL PHTVLTFF+FLEQ+ K +
Sbjct: 235 GVFHCAVETAKL-GPQAFFKGLVPAGVRLVPHTVLTFFMFLEQLRKHF 280

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
Posted date: Jul 30, 2004 1:18 AM
Number of letters in database: 658,882,765
Number of sequences in database: 1,958,132

Lambda K H
0.323 0.138 0.404

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 77,105,680

Number of Sequences: 1958132

Number of extensions: 3159858

Number of successful extensions: 9253

Number of sequences better than 10.0: 343

Number of HSP's better than 10.0 without gapping: 191

Number of HSP's successfully gapped in prelim test: 152

Number of HSP's that attempted gapping in prelim test: 6952

Number of HSP's gapped (non-prelim): 1009

length of query: 314

length of database: 658,882,765

effective HSP length: 125

effective length of query: 189

effective length of database: 414,116,265

effective search space: 78267974085

effective search space used: 78267974085

T: 11

A: 40

X1: 16 (7.5 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (22.0 bits)

S2: 74 (33.1 bits)



Nucleotide

Protein

formatting **BLAST**

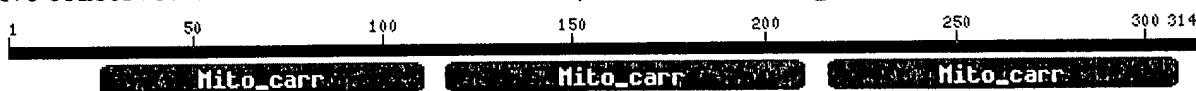
Translations

Retrieve results for an
RID

Your request has been successfully submitted and put into the Blast Queue.

Query = gi|3387911 (314 letters)

Putative conserved domains have been detected, click on the image below for detailed results.



The request ID is 1091209372-21435-212177256124.BLASTQ4

Format! or **Reset all**

The results are estimated to be ready in 25 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi Alignment ☐ in

Use new formatter ☐ Masking Character Default(X for protein, n for nucleotide) ☐ Masking Color Black ☐

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.001

Limit results by or select from: All organisms

Expect value range:



NCBI Conserved Domain Search

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[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Structure](#)
[CDD](#)
[Taxonomy](#)
[Help?](#)

RPS-BLAST 2.2.9 [May-01-2004]

Query= local sequence:
(314 letters)

Database: cdd.v2.00

Click on boxes for multiple alignments



Show

Domain Relatives

PSSMs producing significant alignments:

Score E
(bits) value

gnl CDD 25417	pfam00153, Mito_carr, Mitochondrial carrier protein	76.1	6e-15
gnl CDD 25417	pfam00153, Mito_carr, Mitochondrial carrier protein	75.7	6e-15
gnl CDD 25417	pfam00153, Mito_carr, Mitochondrial carrier protein	73.4	3e-14

[gnl|CDD|25417](#), pfam00153, Mito_carr, Mitochondrial carrier protein.

CD-Length = 96 residues, 89.6% aligned
Score = 76.1 bits (187), Expect = 6e-15

Query:	25	FLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTREYKTSFHALTSILKAEGLRGIYTGL	84
Sbjct:	9	LLAGGIAGAIAATVTYPLDVVKTRLQSAAAGGSRK-YKGILDAFKKIYKEEGIRGLYKGL	67
Query:	85	SAGLLRQATYTTTRLGIYTVLFRLTG	111
Sbjct:	68	GPTLLRVAPYAAIYFGTYEQLKKLLK	94

[gnl|CDD|25417](#), pfam00153, Mito_carr, Mitochondrial carrier protein.

CD-Length = 96 residues, 96.9% aligned
Score = 75.7 bits (186), Expect = 6e-15

Query:	216	SDNILCHFCASMISGLVTTAASMPVDIAKTRIQNMRMIDGKPEYKNGLDVLFKVVRYEFGF	275
Sbjct:	2	PLSFLASLLAGGIAGAIAATVTYPLDVVKTRLQSAA-AGGSRKYKGILDAFKKIYKEEGI	60
Query:	276	FSLWKGFPTPYARLGPHTVLTFFLEQMNKAYKR	309
Sbjct:	61	RGLYKGLGPTLLRVAPYAAIYFGTYEQLKKLLK	94

[gnl|CDD|25417](#), pfam00153, Mito_carr, Mitochondrial carrier protein.

CD-Length = 96 residues, 96.9% aligned
Score = 73.4 bits (180), Expect = 3e-14

Query: 116 PPGFLLKAVIGMTAGATGAFVGTPEVALIRMTADGRLPADQRRGYKNVFNALIRITREE 175
Sbjct: 2 PLSFLASLLAGGIAGAIAATVTYPLDVVKTRLQ---SAAAGGSRKYGILDAFKKIYKEE 58

Query: 176 GVLTLWRGCIPTMARAVVVNAAQLASYSQSKQFLLD 211
Sbjct: 59 GIRGLYKGLGPTLLRVAPYAAIYFGTYEQLKKLLLK 94

Citing CD-Search: Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S, Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen PA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, and Bryant SH (2003), "*CDD: a curated Entrez database of conserved domain alignments*", **Nucleic Acids Res.** 31:383-387.

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